

Table S1. Prenatal sulforaphane-altered lung genes in Nrf2^{-/-} mice (n=523, moderated T-Test, P<=0.01)

RIKEN cDNA and predicted genes excluded. Fold Change (FC): Blue (-) - fold lower in SFN than PBS, Red - fold higher in SFN than PBS.

[ICR, Air, PBS]	[ICR, Air, SFN]	[ICR, O2, PBS]	[ICR, O2, SFN]	RefSeq Transcript ID p	FC Air-PBS:Air-SFN	Gene Symbol	Gene Title	Gene Ontology
31.70388	211.04439	139.37938	102.874115	NM_008318// <i>XXM_c</i>	0.003	6.85 <i>Ibsp</i>	integrin binding sialoprotein	0001503 // ossification // inferred from electronic annotation//0001649 // osteoblast differentiati
85.06954	466.24686	82.19377	71.79115	NM_007802// <i>XXM_c</i>	0.007	5.31 <i>Ctsk</i>	cathepsin K	0001957 // intramembranous ossification // inferred from electronic annotation//0006508 // prot
95.98294	120.96214	65.48201	124.95033	NM_019496	0.004	2.18 <i>Annmcrc1</i>	Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region gene 1	0005515 // protein binding // inferred from electronic annotation
46.458015	95.48914	56.458	47.88668	NM_054084// <i>XXM_c</i>	0.005	2.07 <i>Calcb</i>	caltonin-related peptidase, beta	0042311 // vasodilation // inferred from electronic annotation
140.88501	306.8137	464.6552	672.98926	NM_001291892// <i>XXM_c</i>	0.000	2.05 <i>Gp49a//Lilrb4</i>	glycoprotein 49 A//leukocyte immunoglobulin-like receptor, subfamily B, member 4	0002376 // immune system process // inferred from electronic annotation
75.313576	154.99268	101.2082	145.34927	NR_002870// <i>NR_02</i>	0.007	2.01 <i>Dnm3os//Mir214</i>	dynamins 3, opposite strand//microRNA 214	0001501 // skeletal system development // inferred from mutant phenotype//0003323 // type B f
53.794945	95.00381	121.75727	125.865616	NM_144783	0.001	1.79 <i>Wt1</i>	Wilms tumor 1 homolog	0001222 // negative regulation of transcription from RNA polymerase II promoter // not recorded,
121.42094	227.32707	274.37772	248.9197	NM_001081287// <i>XXM_c</i>	0.008	1.77 <i>Mpp7</i>	membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)	0001334 // positive regulation of protein complex assembly // not recorded//0070830 // tight jun
794.10046	1420.3386	1273.9543	1594.5337	NM_009778	0.002	1.74 <i>C3</i>	complement component 3	0001798 // positive regulation of type IIa hypersensitivity // inferred from mutant phenotype//000
60.04707	104.37409	127.874115	56.07898	NM_177595	0.002	1.74 <i>Mkx</i>	mohawk homeobox	0001222 // negative regulation of transcription from RNA polymerase II promoter // inferred from
109.92215	196.53908	159.87926	241.24054	NM_001081342// <i>XXM_c</i>	0.008	1.72 <i>Gpr133</i>	G protein-coupled receptor 133	0007166 // cell surface receptor signaling pathway // inferred from electronic annotation//000718
43.92867	72.22747	69.90488	143.80573	NM_010111// <i>XXM_c</i>	0.000	1.69 <i>Egr2</i>	early growth response 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regu
51.605183	85.341324	38.49855	69.14183	NM_001112798// <i>XXM_c</i>	0.004	1.69 <i>Slc8a1</i>	solute carrier family 8 (sodium/calcium exchanger), member 1	0001666 // response to hypoxia // not recorded//0001892 // embryonic placenta development //
70.13851	120.759285	70.42109	71.732956	NM_013549// <i>XXM_c</i>	0.001	1.69 <i>Hist2h2aa1//Hist2h2aa2</i>	histone cluster 2, H2aa1//histone cluster 2, H2aa2	0006334 // nucleosome assembly // inferred from electronic annotation//0006334 // nucleosome
519.179	912.1046	993.2537	1059.4312	NM_001099634// <i>XXM_c</i>	0.001	1.69 <i>Myof</i>	myoferlin	0001778 // plasma membrane repair // inferred from mutant phenotype//0006906 // vesicle fusic
24.761656	38.52286	28.732605	40.1172	NM_001164493	0.001	1.67 <i>Klhl29</i>	kelch-like 29	0005515 // protein binding // inferred from electronic annotation
28.037014	43.627186	13.981073	24.802511	NM_001271019// <i>XXM_c</i>	0.002	1.66 <i>Siglec5</i>	sialic acid binding Ig-like lectin 5	0007155 // cell adhesion // inferred from electronic annotation
61.26334	101.78379	89.497955	107.2649	NM_133350// <i>XXM_c</i>	0.001	1.66 <i>Moprc3</i>	microtubule-associated protein, RP/EB family, member 3	0007049 // cell cycle // inferred from electronic annotation//0007067 // mitotic nuclear division /
17.816998	27.668245	19.271816	33.47256	NM_001081221// <i>XXM_c</i>	0.003	1.65 <i>Erc6</i>	excision repair cross-complementing rodent repair deficiency, complementation group 6	0003033 // response to superoxide // inferred from mutant phenotype//0006200 // ATP catabolic
339.01733	580.95264	391.6923	666.7519	NM_027707// <i>XXM_c</i>	0.004	1.64 <i>Nipbl</i>	Nipped-B homolog (Drosophila)	0001222 // negative regulation of transcription from RNA polymerase II promoter // not recorded,
50.261966	79.81739	67.7412	78.21371	NM_001033820// <i>XXM_c</i>	0.008	1.63 <i>Zfp551</i>	zinc finger protein 551	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
75.56271	124.41099	152.30849	150.44853	NM_007562	0.002	1.62 <i>Bnc1</i>	basonuclin 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regu
20.405077	30.765308	14.209172	25.667747	NM_001164785// <i>XXM_c</i>	0.001	1.62 <i>Adamts20</i>	a disintegrin-like and metalloproteinase (reprolysin type) with thrombospondin type 1 motif, 20	0006508 // proteolysis // inferred from direct assay//0007229 // integrin-mediated signaling path
234.03123	397.14606	314.74744	394.0639	NM_030206	0.002	1.62 <i>Cygb</i>	cytoglobin	0006810 // transport // inferred from electronic annotation//0006979 // response to oxidative str
52.2494	81.80647	259.31113	247.28572	NM_009704	0.006	1.60 <i>Areg</i>	amphiregulin	0007173 // epidermal growth factor receptor signaling pathway // not recorded//0007186 // G-pr
125.02729	208.29207	171.68842	333.72653	NM_175406	0.003	1.59 <i>Atp6v0d2</i>	ATPase, H ⁺ -transporting, lysosomal V0 subunit D2	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred
1158.877	1873.5059	1495.2028	1955.8738	NM_001025387// <i>XXM_c</i>	0.002	1.59 <i>Brd2</i>	bromodomain containing 2	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred
107.42899	176.12843	235.57437	467.25763	NM_001281929// <i>XXM_c</i>	0.005	1.57 <i>Gria3</i>	glutamate receptor, ionotropic, AMPA3 (alpha 3)	0006200 // ATP catabolic process // inferred from electronic annotation//0006325 // chromatin o
53.70051	83.161995	52.959114	67.9727	NM_001033371// <i>XXM_c</i>	0.008	1.57 <i>Lrrc36</i>	leucine rich repeat containing 36	0003676 // nucleic acid binding // inferred from electronic annotation//0005515 // protein bindin
262.46674	431.30695	211.01021	359.76227	NM_001110843// <i>XXM_c</i>	0.005	1.56 <i>Cacna2d1</i>	calcium channel, voltage-dependent, alpha2/delta subunit 1	0001666 // response to hypoxia // not recorded//0006081 // cellular aldehyde metabolic process,
35.89475	73.72552	60.431572	51.67067	NM_010408// <i>XXM_c</i>	0.007	1.56 <i>Hcn1</i>	hyperpolarization-activated, cyclic nucleotide-gated K ⁺ 1	0002027 // regulation of heart rate // inferred from mutant phenotype//0006351 // transcription,
663.3817	1061.6375	529.50555	865.80786	NM_145979// <i>XXM_c</i>	0.008	1.55 <i>Chd4</i>	chromodomain helicase DNA binding protein 4	0001525 // angiogenesis // inferred from electronic annotation//0001550 // ovarian cumulus exps
84.82471	132.87904	99.08483	89.56542	NM_198886// <i>XXM_c</i>	0.009	1.53 <i>Zbtb12</i>	zinc finger and BTB domain containing 12	0031581 // hemidesmosome assembly // inferred from sequence or structural similarity//0003158
35.902283	52.35833	35.146736	43.93301	NM_001112725// <i>XXM_c</i>	0.001	1.53 <i>Aldh3a1</i>	aldehyde dehydrogenase family 3, subfamily A1	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred
663.62335	1053.6553	966.693	1393.5911	NM_018826	0.004	1.53 <i>Irx5</i>	Iroquois related homeobox 5 (Drosophila)	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred
21.249775	30.12115	66.71911	94.42819	NM_007950	0.004	1.52 <i>Ereg</i>	epiregulin	0006897 // endocytosis // inferred from electronic annotation
31.079636	44.432465	28.631624	20.66898	NM_001290825// <i>XXM_c</i>	0.000	1.52 <i>Col17a1</i>	collagen, type XVII, alpha 1	0046872 // metal ion binding // inferred from electronic annotation
51.396664	75.82202	73.33496	125.07883	NM_013825	0.003	1.51 <i>Ly75</i>	lymphocyte antigen 75	0001558 // regulation of cell growth // inferred from genetic interaction//0001649 // osteoblast d
24.25811	33.944386	30.495024	36.866108	NM_027425// <i>XXM_c</i>	0.004	1.51 <i>Rufy2</i>	RUN and FYVE domain-containing 2	0016020 // membrane // inferred from electronic annotation//0016021 // integral component of
1153.3927	1767.9536	1137.417	1414.4901	NM_010518	0.004	1.49 <i>Igf1bp5</i>	insulin-like growth factor binding protein 5	0016020 // membrane // inferred from electronic annotation//0016021 // integral component of
290.9779	454.98215	355.3063	526.86945	NM_001033155// <i>XXM_c</i>	0.003	1.49 <i>1110018F16Rik//Dnajb1</i>	RIKEN cDNA 1110018F16 gene//DnaJ (Hsp40) homolog, subfamily B, member 14	0006614 // SRP-dependent cotranslational protein targeting to membrane // inferred from electroi
33.810482	47.470654	38.702503	32.906536	NM_029360	0.001	1.49 <i>Tms4f5</i>	transmembrane 4 superfamily member 5	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred
535.4431	832.6205	311.0486	563.9149	NM_172471// <i>XXM_c</i>	0.009	1.49 <i>Itih5</i>	inter-alpha (globulin) inhibitor H5	0045600 // positive regulation of fat cell differentiation // inferred from mutant phenotype
122.8398	190.98245	185.37529	149.05247	NM_021719	0.005	1.48 <i>Cldn15</i>	claudin 15	0001332 // establishment of mitotic spindle orientation // inferred from genetic interaction//0001
19.760483	27.25687	23.63514	21.806305	NR_040389	0.004	1.48 <i>Gm10785</i>	predicted gene 10785	0002376 // immune system process // inferred from electronic annotation//0009615 // response 1
51.851913	74.192406	75.76936	96.692184	NM_027519// <i>XXM_c</i>	0.010	1.47 <i>Medog</i>	mesenteric estrogen dependent adipogenesis	0002376 // immune system process // inferred from electronic annotation//0006164 // purine nu
1821.1898	2690.7188	2351.985	2372.9458	NM_011896// <i>XXM_c</i>	0.003	1.46 <i>Spry1</i>	sprouty homolog 1 (Drosophila)	0009749 // response to glucose // inferred from mutant phenotype//0003073 // insulin secretion
99.25308	150.39975	162.50865	308.29987	NM_008331	0.003	1.46 <i>Ifit1</i>	interferon-induced protein with tetratricopeptide repeats 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regu
93.340866	140.65144	101.4492	182.96014	NM_011854// <i>XXM_c</i>	0.008	1.46 <i>Oas2</i>	2'-5' oligoadenylate synthetase-like 2	0001702 // gastrulation with mouth forming second // inferred from genetic interaction//0001944
108.7908	164.34299	176.71744	205.29285	NM_001164528// <i>XXM_c</i>	0.004	1.45 <i>Ildr2</i>	immunoglobulin-like domain containing receptor 2	0006468 // protein phosphorylation // not recorded//0006954 // inflammatory response // inferri
115.71432	176.6755	192.81125	243.64786	NM_001081678// <i>XXM_c</i>	0.010	1.45 <i>Zfp800</i>	zinc finger protein 800	0045747 // positive regulation of Notch signaling pathway // not recorded//0051604 // protein m
73.61993	106.82851	97.119835	129.07304	NR_033228	0.002	1.44 <i>E030024N20Rik</i>	peptidylprolyl isomerase A pseudogene 8	0001501 // skeletal system development // inferred from mutant phenotype//0001649 // osteobi
55.95613	79.1136	63.943695	60.61627	NM_008513// <i>XXR_3i</i>	0.003	1.44 <i>Lrp5</i>	low density lipoprotein receptor-related protein 5	0007049 // cell cycle // inferred from electronic annotation//0007059 // chromosome segregati
96.959724	144.30843	102.93956	131.93976	NM_001290374// <i>XXM_c</i>	0.003	1.44 <i>Camk1d</i>	calcium/calmodulin-dependent protein kinase 1D//Mus musculus calcium/calmodulin-dependent protein kin	0006479 // protein methylation // not recorded//0006555 // methionine metabolic process // not
240.132	364.36948	373.0754	511.6522	NM_019571// <i>NR_1</i>	0.001	1.44 <i>Tspan5</i>	tetraspanin 5	0006397 // mRNA processing // inferred from electronic annotation//0006417 // regulation of tra
58.78554	82.877174	79.60454	80.72896	NM_001145920// <i>XXM_c</i>	0.007	1.44 <i>Runx2</i>	runx related transcription factor 2	0007249 // l-kappaB kinase/NF-kappaB signaling // not recorded//0007249 // l-kappaB kinase/NF-
128.53464	193.86139	74.97245	108.28588	NM_029617// <i>XXM_c</i>	0.003	1.44 <i>Casc5</i>	cancer susceptibility candidate 5	0001701 // in utero embryonic development // inferred from genetic interaction//0006351 // tran
108.6009	162.08821	148.47493	120.50201	NM_001081128// <i>XXM_c</i>	0.002	1.43 <i>Mtr</i>	5-methyltetrahydrofolate-homocysteine methyltransferase	0001889 // liver development // not recorded//0006810 // transport // inferred from electronic a
20.343548	27.066057	26.439373	34.410282	NM_001252525// <i>XXM_c</i>	0.002	1.43 <i>Cpeb1</i>	cytoplasmic polyadenylation element binding protein 1	0001556 // oocyte maturation // inferred from direct assay//0001556 // oocyte maturation // infe
33.69915	45.400394	22.629398	34.614645	NM_001081280// <i>XXM_c</i>	0.005	1.42 <i>Nlr3</i>	NLR family, CARD domain containing 3	0001666 // response to hypoxia // inferred from mutant phenotype//0001764 // neuron migrati
230.39433	343.12134	466.976	559.3078	NM_010755// <i>XXM_c</i>	0.005	1.41 <i>Moif</i>	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein F (avian)	0030225 // macrophage differentiation // inferred from direct assay
1920.3824	2765.61	2477.2646	3721.227	NM_010515	0.006	1.41 <i>Igf2r</i>	insulin-like growth factor 2 receptor	0007173 // epidermal growth factor receptor signaling pathway // not recorded//0008284 // posi
498.26935	732.86304	308.37607	466.8467	NM_025995	0.009	1.41 <i>Fbxo5</i>	F-box protein 5	0001843 // neural tube closure // inferred from mutant phenotype//0016567 // protein ubiquitin
110.15724	160.86676	88.89565	112.38599	NM_001139509// <i>XXM_c</i>	0.003	1.41 <i>Nr4a2</i>	nuclear receptor subfamily 4, group A, member 2	0001656 // metanephros development // inferred from expression pattern//0006355 // regulator
67.21004	93.98363	74.082115	79.895386	NM_181584	0.001	1.40 <i>Gab3</i>	growth factor receptor bound protein 2-associated protein 3	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred
120.54283	176.19016	155.63914	176.87526	NM_001033445	0.007	1.40 <i>Gareml</i>	GRB2 associated, regulator of MAPK1	0001665 // MAPK cascade // not recorded//0000165 // MAPK cascade // inferred from sequenc
18.478449	24.167439	22.991898	24.761549	NR_027799	0.009	1.40 <i>Tbrg3</i>	transforming growth factor beta regulated gene 3	0007155 // cell adhesion // inferred from electronic annotation//0016337 // single organismal cell
1700.2263	2398.7046	1773.6273	2308.3413	NM_144788// <i>XXM_c</i>	0.002	1.40 <i>Hectd1</i>	HECT domain containing 1	0001822 // kidney development // inferred from mutant phenotype//0016055 // Wnt signaling pa
634.7859	914.78436	806.3221	716.2482	NM_010574// <i>XXM_c</i>	0.009	1.39 <i>Irx2</i>	Iroquois related homeobox 2 (Drosophila)	0001570 // vasculogenesis // inferred from mutant phenotype//0001649 // osteoblast differenti
37.547443	48.687748	36.727787	52.63854	NM_0008069// <i>XXM_c</i>	0.006	1.37 <i>Gabrb1</i>	gamma-aminobutyric acid (GABA) A receptor, subunit beta 1	0008033 // tRNA processing // inferred from electronic annotation//0032259 // methylation // inf
30.193584	39.033688	51.984455	73.03613	NR_037986	0.004	1.37 <i>Gm16880</i>	predicted gene, 16880	0001508 // action potential // inferred from mutant phenotype//0006810 // transport // inferred
26.211935	33.26756	20.40155	28.361856	NM_009129// <i>XXM_c</i>	0.003	1.37 <i>Scg2</i>	secretogranin II	
155.71693	224.41743	301.37192	276.14014	NM_007962// <i>XXM_c</i>	0.005	1.36 <i>Mpl2</i>	myelin protein zero-like 2	
304.30743	431.4746	343.19257	380.7025	NM_175179	0.007	1.35 <i>Amer1</i>	APC membrane recruitment 1	
29.832485	37.8058	31.621458	33.00762		0.006	1.35 <i>D2Erd127e</i>	DNA segment, Chr 2, ERATO Doi 127, expressed	
176.1112	247.93913	411.68637	526.9774	NM_008416	0.003	1.33 <i>Junb</i>	jun B proto-oncogene	
32.19717	40.597176	30.035881	34.					

[ICR, Air, PBS]	[ICR, Air, SFN]	[ICR, O2, PBS]	[ICR, O2, SFN]	[RefSeq Transcript ID p	FC Air-PBS:Air-SFN	Gene Symbol	Gene Title	Gene Ontology
250.47769	351.10553	385.72855	523.9787	NM_019570//XM_C	0.007	1.33 Rev1	REV1 homolog (S. cerevisiae)	0006260 // DNA replication // inferred from electronic annotation//0006261 // DNA-dependent D
301.80273	418.89847	454.75003	478.62057	NM_011150//XM_C	0.005	1.32 Lgals3bp	lectin, galactoside-binding, soluble, 3 binding protein	0006898 // receptor-mediated endocytosis // inferred from sequence or structural similarity//000
204.62753	287.6124	214.9759	330.38858	NM_028013//XM_C	0.004	1.32 Endod1	endonuclease domain containing 1	0008152 // metabolic process // inferred from electronic annotation//0090305 // nucleic acid pho
227.09082	318.25958	104.60873	192.18773	NM_001033331//N	0.004	1.32 Gas2l3	growth arrest-specific 2 like 3	0000226 // microtubule cytoskeleton organization // not recorded//0007050 // cell cycle arrest //
44.12032	55.75253	58.89628	70.18821	NM_145838//XM_C	0.005	1.32 St8sia6	ST8 alpha-N-acetyl-neuraminidase alpha-2,8-sialyltransferase 6	0001574 // ganglioside biosynthetic process // inferred from direct assay//0006486 // protein glyco
763.9995	1039.4465	821.5112	980.9611	NM_001001602//N	0.010	1.32 Dab2ip	disabled 2 interacting protein	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//
151.4919	210.18614	245.40456	208.30515	NM_001083903//N	0.007	1.32 Sbsn	suprabasin	0005576 // extracellular region // inferred from electronic annotation//0005737 // cytoplasm // i
163.18095	227.16814	176.77748	175.95743	NM_026551//XM_C	0.004	1.32 Dcokd	dephospho-CoA kinase domain containing	0015937 // coenzyme A biosynthetic process // inferred from electronic annotation//0016310 // p
27.693193	34.011208	14.233391	19.101377	NR_024720	0.006	1.31 2700099C18rik	NDC80 homolog, kinetochore complex component pseudogene	
334.70303	459.27002	367.51053	524.10925	NM_127771//XM_C	0.007	1.31 Dmxl2	Dmx-like 2	0005515 // protein binding // inferred from electronic annotation//0017137 // Rab GTPase bindin
196.89948	272.05154	185.8761	346.56134	NM_001170853//XI	0.009	1.31 Mndol//Hf204//Hf205//	myeloid nuclear differentiation antigen like//interferon activated gene 204//interferon activated gene 205/	0030308 // negative regulation of cell growth // inferred from mutant phenotype//0035458 // cell
893.774	1192.8127	2710.3591	1236.5773	NM_018857//XM_C	0.008	1.31 Msln	mesothelin	0007155 // cell adhesion // inferred from electronic annotation//0031016 // pancreas developme
549.282	746.8871	615.7252	833.2459	NM_153178	0.008	1.31 Ago2	argonate RISC catalytic subunit 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regu
213.62871	296.5488	215.08699	266.39948	NM_198035	0.006	1.31 Zbtb39	zinc finger and BTB domain containing 39	0003676 // nucleic acid binding // inferred from electronic annotation//0005515 // protein bindin
160.46207	220.5536	441.01245	337.7131	NM_001083894//N	0.008	1.30 Liph	lipase, member H	0006629 // lipid metabolic process // inferred from electronic annotation//0016042 // lipid catabo
501.0726	676.94775	485.26706	606.8007	NM_001122730//N	0.007	1.30 Trnc18	trinucleotide repeat containing 18	0003677 // DNA binding // inferred from electronic annotation//0003682 // chromatin binding // i
55.226788	70.06314	70.15251	85.027565	XR_105200//XR_10	0.010	1.30 BC035532//Gm17491	Mus musculus, clone IMAGE:5367487, mRNA,///predicted gene, 17491	
206.10951	282.24988	240.04082	364.49112	NM_029639	0.004	1.30 Plet1	placenta expressed transcript 1	0001953 // negative regulation of cell-matrix adhesion // inferred from mutant phenotype//00301
501.13324	675.79376	576.03375	685.29565	NM_001080548//N	0.006	1.29 Usp6nl	USP6 N-terminal like	0007030 // Golgi organization // not recorded//0032313 // regulation of Rab GTPase activity // inf
96.074905	126.52572	159.44437	143.65504	NM_001177752//N	0.009	1.28 Pfkfb3	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3	0006000 // fructose metabolic process // inferred from electronic annotation//0006003 // fructos
31.6456	38.039135	33.43079	31.33232	NR_045294	0.008	1.27 Gm4285	predicted gene 4285	
198.94254	396.924	427.09717	403.13385	NM_011212//XM_C	0.009	1.27 Ptprc	protein tyrosine phosphatase, receptor type, E	0006470 // protein dephosphorylation // inferred from electronic annotation//0007185 // transm
294.51923	392.93863	367.21036	450.61218	NM_001136104//N	0.010	1.27 Abi2	v-abl Abelson murine leukemia viral oncogene 2 (arg, Abelson-related gene)	0006468 // protein phosphorylation // inferred from direct assay//0007015 // actin filament orga
99.18277	129.61693	88.33103	116.8694	NM_145628//XM_C	0.009	1.27 Usp11	ubiquitin specific peptidase 11	0006508 // proteolysis // not recorded//0006511 // ubiquitin-dependent protein catabolic proces
510.08077	593.1886	537.6023	536.623	NM_001145813//N	0.006	1.27 Elf5	E74-like factor 5	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regu
72.91295	92.655815	76.369606	76.22667	NM_022983	0.009	1.27 Lpar3	lysophosphatidic acid receptor 3	0000187 // activation of MAPK activity // inferred from direct assay//0007165 // signal transducti
25.381077	29.784544	24.001633	26.74695	XR_378441//XR_40	0.008	1.26 Sox6os	SRY (sex determining region Y)-box 6, opposite strand	
312.76343	408.10086	488.70282	568.8412	NM_010756//XM_C	0.010	1.25 Mdfg	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein G (avian)	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from
176.90018	148.58652	172.05162	162.12796	NM_212483//XM_C	0.010	-1.24 Krt42	keratin 42	0005198 // structural molecule activity // inferred from electronic annotation
112.08529	91.94309	105.989075	93.89197	NM_015808	0.009	-1.25 Krtap5-1	keratin associated protein 5-1	0005882 // intermediate filament // inferred from electronic annotation//0045095 // keratin filam
55.690758	42.86803	64.70021	59.89046	NM_183087//XM_C	0.010	-1.25 Fam189a1	family with sequence similarity 189, member A1	0006520 // membrane // inferred from electronic annotation//0016021 // integral component of
248.18642	208.43869	228.58908	211.73468	NM_157175	0.009	-1.25 Plekhj2	pleckstrin homology domain containing, family F (with FYVE domain) member 2	0006810 // transport // inferred from electronic annotation//0015031 // protein transport // infer
75.543655	59.731426	70.21141	69.80537	NM_001256005//N	0.009	-1.25 Gbp4//Gbp8	guanylate binding protein 4//guanylate-binding protein 8	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from
1658.202	1363.8546	1565.1398	1253.9458	NM_001110831//N	0.008	-1.25 Dnpep	aspartyl aminopeptidase	0006508 // proteolysis // inferred from electronic annotation
108.12305	88.27646	98.52483	83.57065	NM_019506	0.010	-1.25 Gdf2	growth differentiation factor 2	0001525 // angiogenesis // not recorded//0001569 // patterning of blood vessels // inferred from
24.755665	18.391495	23.54275	17.694609	NM_008103	0.010	-1.25 Gcm1	glial cells missing homolog 1 (Drosophila)	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regu
420.97266	351.99164	243.6928	215.2877	NM_025566	0.010	-1.26 Tnfrap8l1	tumor necrosis factor, alpha-induced protein 8-like 1	
94.800545	75.86157	94.42467	85.864525	NM_172794//XM_C	0.007	-1.26 Zfp454	zinc finger protein 454	0006355 // regulation of transcription, DNA-templated // not recorded
96.67854	72.077896	79.34672	71.210754	NM_026419//XR_4i	0.009	-1.26 Cct3b//LOC102641402	chymotrypsin-like elastase family, member 38//uncharacterized LOC102641402	0006508 // proteolysis // inferred from electronic annotation
576.9163	479.62076	518.05316	464.18796	NM_133999	0.010	-1.26 Fig4	FIG4 homolog (S. cerevisiae)	0007033 // vacuole organization // inferred from mutant phenotype//0007626 // locomotory behav
127.8414	104.62007	107.02186	99.601685	NM_029383	0.010	-1.26 Cldn22	claudin 22	0016338 // calcium-independent cell-cell adhesion // inferred from sequence or structural similari
647.3494	533.822	553.8348	532.7884	NM_025654//XM_C	0.007	-1.26 Rdm1	RAD52 motif 1	0006281 // DNA repair // inferred from electronic annotation//0006310 // DNA recombination // i
253.92201	210.80324	225.56322	194.11992	NM_010149//XM_C	0.008	-1.26 Epor	erythropoietin receptor	0003007 // heart morphogenesis // traceable author statement//0007165 // signal transduction //
196.90826	162.69772	181.02365	147.56238	NM_001289545//N	0.009	-1.27 Atxn7l2	ataxin 7-like 2	
93.195366	73.56165	90.40237	72.39487	NM_016879	0.010	-1.27 Krt85	keratin 85	0005198 // structural molecule activity // inferred from electronic annotation
127.49215	103.226776	116.942314	112.266106	NM_011575	0.007	-1.27 Tjfb	trefoil factor 3, intestinal	0043434 // response to peptide hormone // inferred from electronic annotation
17.175562	13.071379	16.109167	15.289264	NM_009216//XM_C	0.009	-1.27 Sstr1	somatostatin receptor 1	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coup
123.08723	99.16563	113.7869	87.01594	NM_001271472//N	0.007	-1.27 Scube1	signal peptide, CUB domain, EGF-like 1	0051260 // protein homooligomerization // not recorded
95.829056	75.649574	81.587975	72.080086	NM_027010	0.006	-1.27 Crypf	crystallin, gamma F	0001654 // eye development // inferred from mutant phenotype
72.24196	55.609127	58.23118	52.30706	NM_020281	0.010	-1.27 Magea7-ps	melanoma antigen, family A, 7, pseudogene	
105.112625	83.908676	100.90135	83.98092	NR_033644	0.006	-1.27 Fut4-ps1	fucosyltransferase 4, pseudogene 1	
135.38937	109.49695	122.37774	120.672905		0.006	-1.27 Gm9817	predicted gene 9817	
98.435875	77.79113	90.10433	82.813156	NM_001286013//N	0.008	-1.28 Dlk2	delta-like 2 homolog (Drosophila)	0045598 // regulation of fat cell differentiation // inferred from direct assay//0045746 // negative
203.02264	166.5764	198.47736	169.81013	NM_016758	0.008	-1.28 Rgs14	regulator of G-protein signaling 14	0006913 // nucleocytoplasmic transport // inferred from direct assay//0006913 // nucleocytoplasi
122.9893	98.98542	144.21889	144.48506	NM_025293//NR_0	0.007	-1.28 Map2k3os	mitogen-activated protein kinase kinase 3, opposite strand	
179.89563	146.35768	145.30615	129.71944	NM_001164504	0.009	-1.28 Rnf165	ring finger protein 165	0000209 // protein polyubiquitination // inferred from direct assay//0007409 // axonogenesis // i
183.17429	148.62523	174.08365	147.92021	NM_029674//XM_C	0.005	-1.28 Got1l1	glutamic-oxaloacetic transaminase 1-like 1	0006520 // cellular amino acid metabolic process // inferred from electronic annotation//0009058
52.171646	38.944023	44.56744	37.63602	NM_001291003//N	0.007	-1.28 Astl	astacin-like metalloendopeptidase (M12 family)	0006508 // proteolysis // not recorded//0007155 // cell adhesion // inferred from mutant phenot
38.084817	28.472347	32.544216	27.684437	NM_001113417//N	0.010	-1.29 Thrb	thyroid hormone receptor beta	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from
158.63492	128.17188	114.1938	98.5476	NM_001014395//XI	0.007	-1.29 Fbxw22	F-box and WD-40 domain protein 22	0005515 // protein binding // inferred from electronic annotation
309.8575	253.10463	347.6294	367.98383	NM_001033332//N	0.007	-1.29 Tmtc3	transmembrane and tetratricopeptide repeat containing 3	0009791 // post-embryonic development // inferred from mutant phenotype//0010468 // regulat
219.79932	179.45233	271.2101	212.0827	NM_011659//XM_C	0.005	-1.29 Tnfrsf4	tumor necrosis factor receptor superfamily, member 4	0006954 // inflammatory response // inferred from mutant phenotype//0006954 // inflammatory
34.802086	25.539406	25.30799	21.920176	NM_010003	0.004	-1.29 Cyp2c39	cytochrome P450, family 2, subfamily c, polypeptide 39	0055114 // oxidation-reduction process // not recorded
173.29906	139.96109	162.00342	143.08072	NM_001164787//N	0.009	-1.29 Spr2a1//Spr2a2//Sprs	small proline-rich protein 2A1//small proline-rich protein 2A2//small proline-rich protein 2A3	0008360 // regulation of cell shape // traceable author statement//0008544 // epidermis developi
90.01554	69.47447	76.992645	62.95424	NM_138942	0.005	-1.29 Dbh	dopamine beta hydroxylase	0001816 // cytokine production // inferred from mutant phenotype//0001974 // blood vessel rem
102.199936	80.10488	86.653336	71.46167	NM_001286005//N	0.008	-1.29 Abcg8	ATP-binding cassette, sub-family G (WHITE), member 8	0006200 // ATP catabolic process // not recorded//0006810 // transport // inferred from electroni
1912.5457	1521.142	1483.6912	1196.3813	NM_001042451//N	0.006	-1.29 Snca	synuclein, alpha	0001774 // microglial cell activation // inferred from mutant phenotype//0001921 // positive regu
278.99896	227.83887	225.8744	223.39742	NM_153778//XR_3	0.008	-1.29 Atoh8	atoh1 homolog 8 (Drosophila)	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regu
147.75407	118.622314	138.62436	103.58865	NM_001146024//N	0.005	-1.29 Zfp444	zinc finger protein 444	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regu
92.82695	71.83231	85.08331	69.96313	NM_153166//XM_C	0.008	-1.29 Cpne5	copine V	0005515 // protein binding // inferred from electronic annotation
298.56296	242.8654	122.60571	131.46358	NM_027975//XM_C	0.004	-1.30 Fam83d	family with sequence similarity 83, member D	0007049 // cell cycle // inferred from electronic annotation//0007067 // mitotic nuclear division //
140.08636	111.52555	123.66003	95.84841	NM_001277891//N	0.008	-1.30 Fkbp6	FK506 binding protein 6	0000413 // protein peptidyl-prolyl isomerization // inferred from direct assay//0006457 // protein
289.1875	235.82529	215.61014	244.2957	NM_011465//XR_3	0.010	-1.30 Spta1	spectrin alpha, erythrocytic 1	0002260 // lymphocyte homeostasis // inferred from mutant phenotype//0006779 // porphyrin-ci
69.31573	52.203815	35.414585	38.15566	NM_029993	0.010	-1.30 Milana	melan-A	0005515 // protein binding // inferred from electronic annotation
726.5355	578.12994	399.21225	448.62024	NM_023716//NR_0	0.005	-1.30 Tubb2a-ps2//Tubb2b	tubulin, beta 2a, pseudogene 2//tubulin, beta 2B class IIb	0001764 // neuron migration // not recorded//0006184 // GTP catabolic process // inferred from
119.47572	94.07049	107.52871	94.3088	NM_010594	0.006	-1.30 Kap	kidney androgen regulated protein	0005576 // extracellular region // inferred from electronic annotation//0005615 // extracellular s
75.21571	56.938393	64.870735	60.996178	NM_001291009//N	0.004	-1.30 Pla2g10	phospholipase A2, group X	0006629 // lipid metabolic process // inferred from electronic annotation//0006644 // phospholip
105.26999	82.063446	99.39066	86.30274	NM_010359	0.005	-1.30 Gstm3	glutathione S-transferase, mu 3	0008152 // metabolic process // inferred from electronic annotation//0035690 // cellular respons
84.331116	64.2512	88.020134	83.82377	NM_177716	0.008	-1.30 Cdc184	coiled-coil domain containing 184	0005737 // cytoplasm // not recorded
52.1203	38.33534	42.99889	35.81575	NM_013513//XM_C	0.009	-1.31 Epb4.2	erythrocyte protein band 4.2	0000902 // cell morphogenesis // inferred from mutant phenotype//0008360 // regulation of cell

[ICR, Air, PBS]	[ICR, Air, SFN]	[r-ICR, O2, PBS]	[ICR, O2, SFN]	[r-RefSeq Transcript ID p	FC Air-PBS:Air-SFN	Gene Symbol	Gene Title	Gene Ontology
212.21895	170.5844	174.9912	169.42062	NM_146257//XM_C	0.004	-1.31 <i>Slc29a4</i>	solute carrier family 29 (nucleoside transporters), member 4	0006810 // transport // inferred from electronic annotation//0015844 // monoamine transport //
167.34294	133.49031	145.18858	113.6582	NM_001159658//N	0.007	-1.31 <i>Aqp12</i>	aquaporin 12	0006810 // transport // inferred from electronic annotation
19.268366	13.963492	15.410205	16.685665	NM_001164682//N	0.004	-1.31 <i>Mpp4</i>	membrane protein, palmitoylated 4 (MAGUK p55 subfamily member 4)	0035418 // protein localization to synapse // inferred from mutant phenotype
854.76196	674.4786	843.9976	619.2106	NM_008026//XM_C	0.010	-1.31 <i>Fil1</i>	Friend leukemia integration 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regu
309.1059	247.5186	133.42593	396.6182	NM_153143	0.005	-1.31 <i>Kctd11</i>	potassium channel tetramerisation domain containing 11	0007049 // cell cycle // inferred from electronic annotation//0007275 // multicellular organismal c
34.855915	25.014982	51.533577	30.060123	NM_001101482//N	0.010	-1.31 <i>Mrap2</i>	metanorcin 2 receptor accessory protein 2	0006112 // energy reserve metabolic process // inferred from mutant phenotype//0007631 // tee
1418.3018	1110.2058	1206.4363	1114.341	NM_018810//XM_C	0.009	-1.32 <i>Mktn1</i>	makorin, ring finger, protein 1	0002009 // protein polyubiquitination // not recorded//0016567 // protein ubiquitination // infer
159.04988	125.36458	166.0116	161.58946	NM_009086//XM_C	0.004	-1.32 <i>Polr1b</i>	polymerase (RNA) I polypeptide B	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006360 // tran
71.58197	53.156208	68.10403	55.51835	NM_009215	0.004	-1.32 <i>Sst</i>	somatostatin	0001101 // response to acid // inferred from electronic annotation//0006972 // hyperosmotic res
202.7817	161.63774	196.9261	174.1229	NM_033175//XM_C	0.003	-1.32 <i>Lce3c</i>	late cornified envelope 3C	0008544 // epidermis development // inferred from electronic annotation
89.825806	67.95884	86.30454	81.59401	NM_011564	0.006	-1.32 <i>Sry</i>	sex determining region of Chr Y	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from
98.94794	75.56101	85.00992	79.62151	NM_001037752	0.009	-1.32 <i>Defb45</i>	defensin beta 45	0006952 // defense response // inferred from electronic annotation//0042742 // defense respons
97.75643	74.36971	95.53492	83.86803	NM_013773	0.008	-1.32 <i>Tcl1b1</i>	T cell leukemia/lymphoma 18, 1	
118.85292	92.06245	100.898254	99.16808	NM_013533//XM_C	0.004	-1.32 <i>Gpr162</i>	G protein-coupled receptor 162	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coup
59.832237	43.624027	56.743343	45.28395	NM_133364//NM_1	0.003	-1.32 <i>Prima1</i>	proline rich membrane anchor 1	0042135 // neurotransmitter catabolic process // inferred from electronic annotation//0051649 //
81.612	61.001537	68.537994	62.277225	NM_026094//XM_C	0.004	-1.32 <i>Atp8b3</i>	ATPase, class I, type 8B, member 3	0006200 // ATP catabolic process // inferred from mutant phenotype//0006810 // transport // inf
112.07336	86.23608	98.88991	77.975	NM_001101507	0.005	-1.32 <i>Clec2l</i>	C-type lectin domain family 2, member L	0030246 // carbohydrate binding // inferred from electronic annotation
234.62373	185.58629	203.69936	243.78697	NM_001162947//N	0.009	-1.33 <i>Nek3</i>	NIMA (never in mitosis gene a)-related expressed kinase 3	0006468 // protein phosphorylation // inferred from direct assay//0007049 // cell cycle // inferre
223.89586	177.10966	209.33241	179.66913	NM_026335	0.008	-1.33 <i>Lce1h</i>	late cornified envelope 1H	0008544 // epidermis development // inferred from electronic annotation
400.4553	317.61584	124.556145	131.25037	NM_001172092//N	0.004	-1.33 <i>Depdc1a</i>	DEP domain containing 1a	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regu
57.976376	41.63485	49.633217	43.989952	NM_001290138//N	0.005	-1.33 <i>Ccdc169</i>	coiled-coil domain containing 169	
119.15712	91.36323	101.499985	112.21039		0.007	-1.33 <i>Proscos</i>	proline synthetase co-transcribed, opposite strand	
1830.4143	1409.4471	1678.2566	1495.0209	NM_001033988//N	0.005	-1.34 <i>Ncoa4</i>	nuclear receptor coactivator 4	0005739 // mitochondrion // inferred from direct assay
634.9861	496.5077	607.4433	555.71094	NM_001159403//N	0.003	-1.34 <i>Nwd1</i>	NACHT and WD repeat domain containing 1	0000166 // nucleotide binding // inferred from electronic annotation//0005524 // ATP binding // i
46.89701	33.35833	38.454548	40.612354	NM_001146002//N	0.004	-1.34 <i>Txdcd2</i>	thioredoxin domain containing 2 (spermatzoa)	0006457 // protein folding // inferred from direct assay//0006662 // glycerol ether metabolic proc
415.41763	327.161	414.8405	318.99298	NM_009362//XM_C	0.005	-1.34 <i>Tjff1</i>	trefoil factor 1	0006950 // response to stress // inferred from electronic annotation//0008285 // negative regulat
74.270355	54.45309	65.70019	62.32263	NM_145227//XM_C	0.010	-1.34 <i>Oas2</i>	2'-5' oligoadenylate synthetase 2	0002376 // immune system process // inferred from electronic annotation//0006164 // purine nu
40.116776	28.177563	34.936478	26.704489	NM_009611	0.009	-1.34 <i>Act17a</i>	actin-like 7a	0005515 // protein binding // inferred from electronic annotation
257.62292	201.16614	233.79413	180.62936	NM_001195088//N	0.003	-1.34 <i>Tmc8</i>	transmembrane channel-like gene family 8	0001558 // regulation of cell growth // not recorded//0006810 // transport // inferred from electr
90.14916	66.56017	79.27893	66.88353	NM_177693//XM_C	0.004	-1.35 <i>Lim2</i>	lens intrinsic membrane protein 2	0002088 // lens development in camera-type eye // inferred from mutant phenotype//0043010 //
144.51654	111.13407	131.40585	112.64854	NM_029937//XM_C	0.005	-1.35 <i>Nup210l</i>	nucleoporin 210-like	0007286 // spermatid development // inferred from mutant phenotype//0060009 // Sertoli cell de
123.47595	93.72944	105.83267	86.591354	NM_027066	0.002	-1.35 <i>Tmem89</i>	transmembrane protein 89	0005634 // nucleus // not recorded//0016020 // membrane // inferred from electronic annotatio
126.65086	96.12836	117.36861	98.869774	NM_022427//XM_C	0.003	-1.35 <i>Gpr88</i>	G-protein coupled receptor 88	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coup
245.21848	190.1479	235.5229	183.3726	NM_026415	0.005	-1.35 <i>Cysrt1</i>	cysteine rich tail 1	0070062 // extracellular vesicular exosome // not recorded
92.37111	68.36415	86.19487	101.24989	NM_019577//XM_C	0.003	-1.35 <i>Ccl24</i>	chemokine (C-C motif) ligand 24	0001938 // positive regulation of endothelial cell proliferation // not recorded//0006935 // chemic
267.4976	207.83537	221.61696	206.91083	NM_033610//XM_C	0.003	-1.35 <i>Sncb</i>	synuclein, beta	0007268 // synaptic transmission // inferred from genetic interaction//0042417 // dopamine met
154.00327	118.55258	146.33069	109.78352	NM_010381//XM_C	0.005	-1.35 <i>H2-Ea-ps</i>	histocompatibility 2, class II antigen E alpha, pseudogene	0002376 // immune system process // inferred from electronic annotation//0002504 // antigen pr
329.50635	256.1405	262.90204	209.00514	NM_009446//NM_C	0.004	-1.35 <i>Tuba3a//Tuba3b</i>	tubulin, alpha 3A//tubulin, alpha 3B	0006184 // GTP catabolic process // inferred from electronic annotation//0007017 // microtubule
570.63544	439.5892	118.77344	795.83356	NM_010240//NR_0	0.004	-1.35 <i>Ftl1//Gm20746//LOC10</i>	ferritin light chain 1//predicted gene, 20746//ferritin light chain 1-like//microRNA 692-1//microRNA 692-2	0006826 // iron ion transport // inferred from electronic annotation//0006879 // cellular iron i
120.8282	91.25962	117.8239	88.65962	NM_028799	0.007	-1.35 <i>Tgm5</i>	transglutaminase 5	0018149 // peptide cross-linking // inferred from electronic annotation
316.18216	246.53752	280.0087	225.70671	NM_007847	0.004	-1.35 <i>Defa-rs2</i>	defensin, alpha, related sequence 2	0006952 // defense response // inferred from electronic annotation//0032496 // response to lipo
114.57776	86.26772	93.530205	82.40197	NM_011139	0.005	-1.36 <i>Pou2f3</i>	POU domain, class 2, transcription factor 3	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regu
768.80475	586.56995	713.0906	581.60895	NM_001037326//N	0.004	-1.36 <i>Cstf3</i>	cleavage stimulation factor, 3' pre-RNA, subunit 3	0006396 // RNA processing // inferred from electronic annotation//0006397 // mRNA processing,
23.973154	16.474997	23.403814	19.023779	NM_001271716//N	0.005	-1.36 <i>Mc2r</i>	melanocortin 2 receptor	0001890 // placenta development // inferred from electronic annotation//0007165 // signal trans
111.86112	83.63365	79.2544	69.56707	NM_054095//XM_C	0.002	-1.36 <i>Necab2</i>	N-terminal EF-hand calcium binding protein 2	0005509 // calcium ion binding // inferred from electronic annotation//0005515 // protein bindi
458.6414	352.86316	424.442	353.3893	NM_011025//XM_C	0.005	-1.36 <i>Oxt</i>	oxytocin	0001975 // response to amphetamine // inferred from electronic annotation//0002027 // regulat
136.53804	103.31054	122.66202	98.57161	NM_010601//XM_C	0.005	-1.36 <i>Kcnh3</i>	potassium voltage-gated channel, subfamily H (eag-related), member 3	0000160 // phosphorelay signal transduction system // inferred from electronic annotation//0006
64.143814	45.74545	51.07201	46.518984	NM_157427//XM_C	0.002	-1.36 <i>Fam163b</i>	family with sequence similarity 163, member B	0016020 // membrane // inferred from electronic annotation//0016021 // integral component of
190.85114	145.67776	180.23357	133.79602	NM_001039049	0.003	-1.37 <i>Cox8c</i>	cytochrome c oxidase subunit VIIIc	1902600 // hydrogen ion transmembrane transport // inferred from electronic annotation
793.64496	602.3772	1253.9342	1009.8993	NM_027464//XM_C	0.008	-1.37 <i>Fam213a</i>	family with sequence similarity 213, member A	0045670 // regulation of osteoclast differentiation // not recorded//0055114 // oxidation-reduct
101.43361	74.699875	103.13095	89.84359	NM_177897//XR_3i	0.002	-1.37 <i>B4galnt4</i>	beta-1,4-N-acetyl-galactosaminyl transferase 4	0008152 // metabolic process // not recorded
109.99309	81.30346	47.028076	54.925083	NM_010883	0.008	-1.38 <i>Ndp</i>	Norrie disease (pseudoglioma) (human)	0001890 // placenta development // inferred from mutant phenotype//0016055 // Wnt signaling
65.868324	46.16065	49.529713	49.381584	NM_022888//NM_1	0.004	-1.38 <i>Folr4</i>	folate receptor 4 (delta)	0007155 // cell adhesion // inferred from mutant phenotype//0007338 // single fertilization // inf
50.97551	35.07701	43.97094	39.995914	NM_177448	0.004	-1.38 <i>Mogat2</i>	monoacylglycerol O-acyltransferase 2	0006071 // glycerol metabolic process // inferred from electronic annotation//0006629 // lipid me
27.947567	18.82351	20.317287	20.69878	NM_011996	0.003	-1.38 <i>Adh4</i>	alcohol dehydrogenase 4 (class II), pi polypeptide	0001523 // retinoid metabolic process // not recorded//0006066 // alcohol metabolic process // n
37.492348	25.617674	33.39885	27.986418	NM_001167879	0.002	-1.38 <i>Gareml</i>	GRB2 associated, regulator of MAPK1-like	
1077.6061	804.4449	967.66095	831.316	NM_026050//NM_1	0.005	-1.39 <i>Fam220a</i>	family with sequence similarity 220, member A	0005634 // nucleus // inferred from electronic annotation
44.142605	29.923456	35.93549	33.383488	NM_001171640	0.009	-1.39 <i>Actl10</i>	actin-like 10	
52.81152	36.34758	58.475872	50.886513	NM_021325	0.009	-1.39 <i>Cd200r1</i>	CD200 receptor 1	0005886 // plasma membrane // inferred from electronic annotation//0009897 // external side of
163.92223	98.174416	126.482025	98.58774	NM_147221//XM_C	0.003	-1.39 <i>Glis1</i>	GLIS family zinc finger 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from
85.20198	60.45209	77.21883	75.55018	NM_001290452//N	0.005	-1.40 <i>Mzf1</i>	myeloid zinc finger 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regu
32.57386	21.949392	26.60658	22.348583	NM_021340//XM_C	0.006	-1.40 <i>Rgr</i>	retinal G-protein coupled receptor	0006935 // chemotaxis // inferred from electronic annotation//0007165 // signal transduction // i
910.95795	672.1001	746.25885	507.74216	NM_146008	0.006	-1.40 <i>Tcp11l2</i>	t-complex 11 (mouse) like 2	0000737 // DNA catabolic process, endonucleolytic // not recorded
185.12082	137.07129	166.49597	140.58675	NM_001172136//N	0.003	-1.41 <i>Exog</i>	endo/exonuclease (5'-3'), endonuclease G-like	0006915 // apoptotic process // inferred from electronic annotation//0007165 // signal transducti
164.9194	121.29307	159.21935	134.45238	NM_001033433	0.002	-1.41 <i>Tmem102</i>	transmembrane protein 102	0007623 // circadian rhythm // not recorded//0008152 // metabolic process // inferred from elect
243.08191	179.99983	216.03056	181.9311	NM_001081327//N	0.001	-1.41 <i>Hs3st2</i>	heparan sulfate (glucosaminyl) 3-O-sulfotransferase 2	0006351 // transcription, DNA-templated // not recorded//0006355 // regulation of transcription,
266.2953	195.99948	226.59492	196.62822	NM_008701//XM_C	0.004	-1.42 <i>Nkx2-9</i>	NK2 homeobox 9	0002084 // protein depalmitoylation // inferred from mutant phenotype//0006629 // lipid metab
729.0145	531.8995	741.53864	542.4106	NM_008866//XM_C	0.009	-1.42 <i>Lypla1</i>	lysophospholipase 1	
28.390142	18.53598	22.333838	19.802942	NM_027072	0.006	-1.43 <i>Plac8l1</i>	PLAC8-like 1	
1052.9667	758.3665	981.7409	635.7656	NM_013772//XM_C	0.001	-1.44 <i>LOC100041483//Tct1b3</i>	protein TCL1B3-like//T cell leukemia/lymphoma 18, 3	0005515 // protein binding // inferred from electronic annotation//0008270 // zinc ion binding //
105.735435	73.71705	115.80032	76.45401	NM_001099632	0.001	-1.45 <i>Rnf39</i>	ring finger protein 39	0008152 // metabolic process // inferred from electronic annotation//0008610 // lipid biosynthe
417.6363	304.8422	316.3287	257.26706	NM_009338//NM_1	0.007	-1.45 <i>Acat2//Acat3</i>	acetyl-Coenzyme A acetyltransferase 2//acetyl-Coenzyme A acetyltransferase 3	
2521.7776	1759.38	2140.292	1843.2498	NM_001142952//Xi	0.010	-1.45 <i>Fam46c</i>	family with sequence similarity 46, member C	0007165 // signal transduction // inferred from electronic annotation//0007399 // nervous system
332.6392	240.5345	273.74942	220.21518	NM_001113246//N	0.009	-1.46 <i>Chn1</i>	chimerin 1	
123.77513	86.37831	112.16693	94.96171		0.002	-1.46 <i>Ai043046</i>	expressed sequence AI043046	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coup
35.13173	22.373497	30.004507	24.36192	NM_008177	0.002	-1.48 <i>Grpr</i>	gastrin releasing peptide receptor	0007262 // STAT protein import into nucleus // inferred from sequence or structural similarity//00
118.34083	81.60523	101.33044	91.47962	NM_001380//XM_C	0.003	-1.48 <i>Il20</i>	interleukin 20	0031072 // heat shock protein binding // inferred from electronic annotation//00051082 // unfold
60.153282	38.781097	45.226504	39.583744	NM_175525//XM_C	0.001	-1.49 <i>Ssu2</i>	ssu-2 homolog (C. elegans)	0006081 // cellular aldehyde metabolic process // inferred from electronic annotation//0008152 //
36.701405	23.111998	31.468988	24.574776	NM_001177438//N	0.005	-1.50 <i>1700055N04Rik//Aldh3b</i>	RIKEN cDNA 1700055N04 gene//aldehyde dehydrogenase 3 family, member B2//aldehyde dehydrogenase 3	0006334 // nucleosome assembly // inferred from electronic annotation
963.528	654.9564	940.2358	716.4789	NM_009433	0.010	-1.52 <i>Tsyp1l</i>	testis-specific protein, Y-encoded-like 1	

[ICR, Air, PBS]	[ICR, Air, SFN]	[ICR, O2, PBS]	[ICR, O2, SFN]	RefSeq Transcript ID	p	FC Air-PBS:Air-SFN	Gene Symbol	Gene Title	Gene Ontology
152.2644	102.52239	134.26436	104.37595	NM_029667	0.001	-1.52	Lce1l	late cornified envelope 1l	0008544 // epidermis development // inferred from electronic annotation
101.94964	66.872055	81.4693	76.863785	NM_001136237//N	0.002	-1.52	Slc39a5	solute carrier family 39 (metal ion transporter), member 5	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred
90.53483	58.597626	54.37917	45.056515	NM_019538//XM_c	0.004	-1.53	Plac1	placental specific protein 1	0001890 // placenta development // inferred from expression pattern//0001890 // placenta devel
66.74981	42.613354	57.500587	50.571495	NM_013797//XM_c	0.004	-1.53	Slco1a1	solute carrier organic anion transporter family, member 1a1	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred
604.0621	408.2919	385.23013	427.03336	NM_145587//XM_c	0.009	-1.54	Sbk1	SH3-binding kinase 1	0006468 // protein phosphorylation // inferred from electronic annotation//0016310 // phosphor
197.70314	132.63347	421.5775	396.7446	NM_010501	0.008	-1.56	Ifit3	interferon-induced protein with tetratricopeptide repeats 3	0002376 // immune system process // inferred from electronic annotation//0008285 // negative r
2791.4875	1792.2322	2109.443	1831.4321	NM_007563//XM_c	0.006	-1.56	Bpgm	2,3-bisphosphoglycerate mutase	0006096 // glycolytic process // inferred from electronic annotation//0008152 // metabolic proce:
124.81598	79.31379	87.99361	72.32608	NM_027292	0.003	-1.60	Tspo2	translocator protein 2	0006810 // transport // inferred from electronic annotation
24.214493	13.980096	20.205318	16.6023	NM_029536	0.001	-1.64	Gpr165	G protein-coupled receptor 165	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coup

Table S2. Prenatal sulforaphane-altered 918 lung genes in postnatal air-exposed *Nrf2*^{-/-} mice (n=918, moderated T-Test, P<=0.01)

RIKEN cDNA and predicted genes excluded. Fold Change (FC): Blue (-) - fold lower in SFN than PBS, Red - fold higher in SFN than PBS.

[Nrf2-KO, Air, PBS]	[Nrf2-KO, Air, SFN]	RefSeq Transcript ID	p	FC PBS:SFN	Gene Symbol	Gene Title	Gene Ontology
248.11972	666.50073	NM_001030294///XN	0.007	2.73	<i>Olfm4</i>	olfactomedin 4	0007155 // cell adhesion // inferred from electronic annotation///0043124 // negative regulation of I-kappaB kinase activity
484.7015	1256.8951	NR_003513	0.000	2.66	<i>Neat1</i>	nuclear paraspeckle assembly transcript 1 (non-protein coding)///---	0030575 // nuclear body organization // inferred from mutant phenotype///0043954 // cellular component maintenance
231.03038	564.68445	NM_144513///NR_0C	0.001	2.46	<i>Meg3</i>	maternally expressed 3///---	0001701 // in utero embryonic development // inferred from mutant phenotype///0001889 // liver development /
919.71274	2061.3145	NM_001082543///NM	0.009	2.33	<i>BC100530///Stfo1</i>	cDNA sequence BC100530///stefin A1	0010466 // negative regulation of peptidase activity // inferred from electronic annotation///0010951 // negative i
30.045393	63.700813	NM_139134///XM_0	0.000	2.04	<i>Chodl</i>	chondrolectin	0005540 // hyaluronic acid binding // inferred from sequence or structural similarity///0030246 // carbohydrate bi
47.849865	102.033646	NM_011410///XM_0	0.001	2.02	<i>Slfn4</i>	schlafen 4	0005524 // ATP binding // inferred from electronic annotation
491.72003	962.13226	NM_023665	0.000	2.00	<i>Rsrp1</i>	arginine/serine rich protein 1	
1075.8644	2057.7217	NM_001042634///NM	0.000	1.98	<i>Clk1</i>	CDC-like kinase 1	0006468 // protein phosphorylation // not recorded///0016310 // phosphorylation // inferred from electronic ann
30.43497	62.552834	NM_001110505///NM	0.000	1.98	<i>Amy1///Rnpc3</i>	amylase 1, salivary///RNA-binding region (RNP1, RRM) containing 3	0005975 // carbohydrate metabolic process // inferred from electronic annotation///0008152 // metabolic proces
83.35101	168.04236	NM_001037743///XN	0.002	1.96	<i>4921506M07Rik///LOC102642336</i>	RIKEN cDNA 4921506M07 gene///tetratricopeptide repeat protein 6-like	0005515 // protein binding // inferred from electronic annotation
521.4066	989.1873	NM_018856///NM_2	0.000	1.93	<i>Ccnl2</i>	cyclin L2	0000079 // regulation of cyclin-dependent protein serine/threonine kinase activity // inferred from electronic ann
48.200565	94.03042	NM_178278///XM_0	0.001	1.84	<i>Caps2</i>	calcyphosphine 2	0005509 // calcium ion binding // inferred from electronic annotation///0046872 // metal ion binding // inferred fi
349.55603	617.0719	NM_144847///XM_0	0.004	1.78	<i>Nrbp2</i>	nuclear receptor binding protein 2	0006468 // protein phosphorylation // inferred from electronic annotation///0007399 // nervous system developm
230.99739	407.30475	NM_009903	0.005	1.77	<i>Clcn4</i>	claudin 4	0007565 // female pregnancy // inferred from electronic annotation///0016338 // calcium-independent cell-cell ac
54.208763	100.84891	NR_015505///NR_02	0.000	1.76	<i>Firre</i>	functional intergenic repeating RNA element	
163.32114	285.9527	NR_015531	0.006	1.75	<i>Dancr</i>	differentiation antagonizing non-protein coding RNA	
51.093113	94.192444	NM_001037743///XN	0.002	1.73	<i>4921506M07Rik///LOC102642336</i>	RIKEN cDNA 4921506M07 gene///tetratricopeptide repeat protein 6-like	0005515 // protein binding // inferred from electronic annotation
47.613567	86.71949	NM_007749	0.005	1.73	<i>Cox7c</i>	cytochrome c oxidase subunit VIIc	1902600 // hydrogen ion transmembrane transport // inferred from electronic annotation
360.36276	616.44116	NM_172779///XM_0	0.000	1.72	<i>Ddx26b</i>	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26B	
406.63916	691.392	NM_001159632///NM	0.000	1.72	<i>Atpv61c2</i>	ATPase, H+ transporting, lysosomal V1 subunit C2	0006200 // ATP catabolic process // inferred from direct assay///0006810 // transport // inferred from electronic a
33.014507	59.086693	NM_172864	0.010	1.72	<i>Wdr63</i>	WD repeat domain 63	0005515 // protein binding // inferred from electronic annotation
314.8336	536.64435	NM_023755///XM_0	0.003	1.72	<i>Tjcp2l1</i>	transcription factor CP2-like 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay///0
396.84558	672.9599	NM_001290533///NM	0.000	1.71	<i>Ogt</i>	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:poly	0006110 // regulation of glycolytic process // not recorded///0006486 // protein glycosylation // inferred from ele
1034.6279	1705.6106	NM_010821///XM_0	0.002	1.70	<i>Mpeg1</i>	macrophage expressed gene 1	0016020 // membrane // inferred from electronic annotation///0016021 // integral component of membrane // in
82.523415	145.46419	NM_175430///XM_0	0.007	1.68	<i>Cdc40</i>	coiled-coil domain containing 40	0001947 // heart looping // not recorded///0003341 // cilium movement // inferred from mutant phenotype///00
118.005165	203.55351	NR_029382///NR_02	0.000	1.68	<i>Mir17hg///Mir92-1</i>	Mir17 host gene 1 (non-protein coding)///microRNA 92-1	0001701 // in utero embryonic development // inferred from genetic interaction///0002329 // pre-B cell differenti
185.878	308.80588	NM_007714///XM_0	0.000	1.65	<i>Clk4</i>	CDC like kinase 4	0006468 // protein phosphorylation // inferred from electronic annotation///0016310 // phosphorylation // infer
433.29846	705.4861	NM_001113136///NM	0.000	1.65	<i>Ptpcr</i>	protein tyrosine phosphatase, receptor type, C	0000187 // activation of MAPK activity // inferred from mutant phenotype///0001915 // negative regulation of T c
863.275	1382.106	NM_025951///NM_0	0.003	1.65	<i>Plk42b</i>	phosphatidylinositol 4-kinase type 2 beta	0016310 // phosphorylation // inferred from electronic annotation///0046854 // phosphatidylinositol phosphoryla
168.4762	278.56406	NM_026985///XM_0	0.003	1.64	<i>Mcomp1</i>	mast cell expressed membrane protein 1	0016020 // membrane // inferred from electronic annotation///0016021 // integral component of membrane // in
156.02037	253.80077	NM_001252401///NM	0.001	1.61	<i>Tle2</i>	transducin-like enhancer of split 2, homolog of Drosophila E(spl)	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transci
18.54299	29.746069	NM_010870///XM_0	0.009	1.60	<i>Naip5</i>	NLR family, apoptosis inhibitory protein 5	0002376 // immune system process // inferred from electronic annotation///0006915 // apoptotic process // infer
87.88481	147.03099	NM_001099633///XN	0.004	1.60	<i>Dnah9</i>	dynein, axonemal, heavy chain 9	0006200 // ATP catabolic process // inferred from electronic annotation///0007018 // microtubule-based moveme
5237.8335	8342.986	NM_001079694///NM	0.002	1.60	<i>Srsf5</i>	serine/arginine-rich splicing factor 5	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transci
224.72978	357.68903	NM_001025566///NM	0.001	1.59	<i>Chka</i>	choline kinase alpha	0006629 // lipid metabolic process // inferred from electronic annotation///0006646 // phosphatidylethanolamine
152.43263	243.70963	NM_010877///XM_0	0.003	1.58	<i>Ncf2</i>	neutrophil cytosolic factor 2	0006742 // NADP catabolic process // not recorded///0006801 // superoxide metabolic process // not recorded///
333.3535	517.65094	NM_026110///XR_38	0.000	1.57	<i>Paxbp1</i>	PAX3 and PAX7 binding protein 1	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transci
319.89084	494.23187	NM_009841	0.002	1.55	<i>Cd14</i>	CD14 antigen	0002237 // response to molecule of bacterial origin // inferred from direct assay///0002376 // immune system pro
353.4351	543.24054	NR_027008///NR_02	0.001	1.55	<i>Gt(ROSA)26Sor</i>	gene trap ROSA 26, Philippe Soriano	
173.75519	271.15042	NM_001159299///NM	0.003	1.55	<i>Itih4</i>	inter alpha-trypsin inhibitor, heavy chain 4	0006953 // acute-phase response // inferred from electronic annotation///0010466 // negative regulation of pepti
1384.8971	2067.0303	NM_007705///XM_0	0.001	1.54	<i>Cirbp</i>	cold inducible RNA binding protein	0006950 // response to stress // inferred from electronic annotation///0009409 // response to cold // inferred fro
540.30457	814.6418	NR_030711	0.000	1.53	<i>Mir22hg</i>	Mir22 host gene (non-protein coding)	
12.886861	19.568853	NM_001085518///NM	0.005	1.52	<i>Gm14085///Sic28a2</i>	predicted gene 14085///solute carrier family 28 (sodium-coupled nucleoside transp	0001895 // retina homeostasis // not recorded///0006810 // transport // inferred from electronic annotation///00
266.34436	405.37885	NM_177268///XM_0	0.001	1.52	<i>Ankrd16</i>	ankyrin repeat domain 16	0005515 // protein binding // inferred from electronic annotation
4281.399	6319.4473	NM_001123037///NM	0.002	1.51	<i>Eif4a2</i>	eukaryotic translation initiation factor 4A2	0006200 // ATP catabolic process // inferred from electronic annotation///0006412 // translation // inferred from
965.78796	1409.3214	NM_023842///XM_0	0.004	1.51	<i>Dsp</i>	desmoplakin	0002934 // desmosome organization // inferred from mutant phenotype///0003223 // ventricular compact myoca
14.523185	21.862753	NR_028555	0.005	1.51	<i>Snord89</i>	small nucleolar RNA, C/D box 89	
47.770977	75.73093	NM_030110///XM_0	0.002	1.51	<i>Micu3</i>	mitochondrial calcium uptake family, member 3	0005509 // calcium ion binding // inferred from electronic annotation///0046872 // metal ion binding // inferred fi
1796.5664	2621.1614	NM_001271538///NM	0.001	1.51	<i>Myh14</i>	myosin, heavy polypeptide 14	0003009 // skeletal muscle contraction // not recorded///0006200 // ATP catabolic process // inferred from direct
146.00955	222.34581	NM_001163489///NM	0.001	1.50	<i>Sema4a</i>	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short	00001525 // angiogenesis // inferred from electronic annotation///0002292 // T cell differentiation involved in imm
324.76068	484.28998	NM_001160378///NM	0.004	1.50	<i>Fam46a</i>	family with sequence similarity 46, member A	0044822 // poly(A) RNA binding // not recorded
59.42976	95.02456	NM_183276	0.000	1.50	<i>Nbeal2</i>	neurobeachin-like 2	0007596 // blood coagulation // inferred from mutant phenotype///0030220 // platelet formation // not recorded
444.4374	659.4524	NM_181595///XM_0	0.003	1.50	<i>Ppp19a</i>	protein phosphatase 1, regulatory (inhibitor) subunit 9A	0007015 // actin filament organization // inferred from physical interaction///0019722 // calcium-mediated signali
37.036602	57.648235	NM_001244617///NM	0.005	1.49	<i>B4galnt1</i>	beta-1,4-N-acetyl-galactosaminyl transferase 1	0001574 // ganglioside biosynthetic process // inferred from genetic interaction///0001574 // ganglioside biosynt
59.582714	94.57021	NR_033641///NR_11	0.002	1.49	<i>Cnde</i>	colorectal neoplasia differentially expressed (non-protein coding)	
221.61835	330.93765	NM_016805///XR_37	0.002	1.49	<i>AI503316///Hnnpnu</i>	expressed sequence AI503316///heterogeneous nuclear ribonucleoprotein U	0001649 // osteoblast differentiation // not recorded///0006397 // mRNA processing // inferred from electronic a
265.57697	395.9591	NM_001163507///NM	0.006	1.49	<i>Mmm1</i>	multimerin 1	0005509 // calcium ion binding // inferred from electronic annotation///0005515 // protein binding // inferred fro
558.2761	815.70386	NM_020008	0.007	1.49	<i>Clec7a</i>	C-type lectin domain family 7, member a	0001878 // response to yeast // inferred from direct assay///0001879 // detection of yeast // inferred from direct
67.38696	106.11947	NM_001037138///NM	0.000	1.49	<i>Cd300lb</i>	CD300 antigen like family member B	0002376 // immune system process // inferred from electronic annotation///0002446 // neutrophil mediated imm
42.761967	66.288	NM_001033371///NM	0.004	1.48	<i>Lrrc36</i>	leucine rich repeat containing 36	
1258.657	1816.5428	NM_008259///XM_0	0.006	1.48	<i>Foxa1</i>	forkhead box A1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenoty
525.38477	761.0276	NM_182995///XM_0	0.001	1.48	<i>Ccp110</i>	centriolar coiled coil protein 110	0007099 // centriole replication // not recorded///0030030 // cell projection organization // inferred from electror
39.66738	61.26164	NM_001081330///NM	0.004	1.47	<i>Dnah2</i>	dynein, axonemal, heavy chain 2	0001539 // cilium or flagellum-dependent cell motility // inferred from electronic annotation///0006200 // ATP cat
138.30579	208.84721	NM_145931///NR_02	0.001	1.47	<i>Zc3h7a</i>	zinc finger CCH type containing 7 A	0005515 // protein binding // inferred from electronic annotation///0044822 // poly(A) RNA binding // not record
88.47535	137.02032	NM_001048148///NM	0.001	1.47	<i>Lime1///Zgpat</i>	Lck interacting transmembrane adaptor 1///zinc finger, CCH-type with G patch do	0002376 // immune system process // inferred from electronic annotation///0006351 // transcription, DNA-templ
113.04274	172.02422	NM_001286037///NM	0.007	1.46	<i>Ncf1</i>	neutrophil cytosolic factor 1	0001878 // response to yeast // inferred from mutant phenotype///0001909 // leukocyte mediated cytotoxicity //
721.21643	1035.0679	NM_001285917///NM	0.005	1.46	<i>Dapk1</i>	death associated protein kinase 1	0006417 // regulation of translation // inferred from electronic annotation///0006468 // protein phosphorylation /
107.57254	163.78413	NM_001169153///NM	0.006	1.46	<i>Cd300lf</i>	CD300 antigen like family member F	0002376 // immune system process // inferred from electronic annotation///0030316 // osteoclast differentiation
1211.1276	1722.7161	NM_001042565///NM	0.002	1.46	<i>Wsb1</i>	WD repeat and SOCS box-containing 1	0016567 // protein ubiquitination // inferred from electronic annotation///0035556 // intracellular signal transduc

[Nrf2-KO, Air, PBS]	[Nrf2-KO, Air, SFN]	RefSeq	Transcript ID	p	FC	PBS:SFN	Gene Symbol	Gene Title	Gene Ontology
420.41507	606.72095	NM_010153		0.001	1.46	Erbb3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	0003197 // endocardial cushion development // inferred from mutant phenotype//0006468 // protein phosphorylation	
65.2575	101.230415	NM_010172//XN_O		0.001	1.45	F7	coagulation factor VII	0002690 // positive regulation of leukocyte chemotaxis // not recorded//0006508 // proteolysis // not recorded//0008333 // endosome to lysosome transport // inferred from genetic interaction//0032313 // regulation of Rab G	
1635.5033	2296.8918	NM_001081066//XN		0.005	1.45	Dennd3	DENN/MADD domain containing 3	0002540 // leukotriene production involved in inflammatory response // inferred from mutant phenotype//00026	
637.93494	906.65656	NM_000963		0.003	1.45	Alox5ap	arachidonate 5-lipoxygenase activating protein	0001525 // angiogenesis // inferred from mutant phenotype//0006351 // transcription, DNA-templated // infer	
605.808	851.91	NM_001083319//NN		0.003	1.44	Ubp1	upstream binding protein 1	0006955 // immune response // inferred from electronic annotation//0010467 // gene expression // inferred from	
263.9472	379.15244	NM_0008518		0.004	1.43	Ltb	lymphotoxin B	0002244 // hematopoietic progenitor cell differentiation // inferred from mutant phenotype//0006910 // phagoc	
269.98145	384.48294	NM_001177646//NN		0.001	1.43	Sirpa	signal-regulatory protein alpha	0005886 // plasma membrane // inferred from electronic annotation//0016020 // membrane // inferred from ele	
895.12146	1246.6874	NM_013706		0.003	1.43	Cd52	CD52 antigen	0006396 // RNA processing // inferred from electronic annotation	
415.05365	588.68115	NM_001033261//XN		0.002	1.43	Zfc3h1	zinc finger, C3H1-type containing	0001122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0	
76.22841	115.73562	NM_001289877//NN		0.002	1.43	Per3	period circadian clock 3	0006915 // apoptotic process // inferred from electronic annotation//0072661 // protein targeting to plasma me	
404.38428	571.02747	NM_001081170//NN		0.003	1.42	Pacs2	phosphofurin acidic cluster sorting protein 2	0005524 // ATP binding // inferred from electronic annotation//0016301 // kinase activity // inferred from electr	
98.16076	146.41182	NM_133898//XN_O		0.009	1.42	N4bp21	NEDD4 binding protein 2-like 1	0008152 // metabolic process // inferred from electronic annotation//0016998 // cell wall macromolecule catabo	
10063.819	13977.084	NM_017372		0.001	1.42	Lyz2	lysozyme 2	0016021 // integral component of membrane // inferred from electronic annotation	
760.2875	1051.3357	NM_001114174//XN		0.002	1.42	Fam189a2	family with sequence similarity 189, member A2	0000165 // MAPK cascade // inferred from direct assay//0000165 // MAPK cascade // not recorded//0000186 //	
319.055	448.22928	NM_008580//XN_O		0.001	1.41	Map3k5	mitogen-activated protein kinase kinase kinase 5	0001822 // kidney development // inferred from mutant phenotype//0006211 // 5-methylcytosine catabolic proc	
402.90393	563.9757	NM_001040400//NN		0.008	1.41	Tet2	tet methylcytosine dioxygenase 2	0005515 // protein binding // inferred from electronic annotation	
272.56906	382.9671	NM_030075//XN_O		0.007	1.41	Klhdcb8	kelch domain containing 8B	0006810 // transport // inferred from electronic annotation	
562.46075	777.54803	NM_010686//XN_O		0.005	1.41	Laptm5	lysosomal-associated protein transmembrane 5	0001505 // regulation of neurotransmitter levels // inferred from mutant phenotype//0001932 // regulation of pr	
1160.15	1591.2454	NM_010091//XN_O		0.006	1.40	Dvl1	dishevelled, dsh homolog 1 (Drosophila)	0005515 // protein binding // inferred from electronic annotation	
1918.7164	2618.1584	NM_001162926//NN		0.002	1.40	Fam84b	family with sequence similarity 84, member B	0001764 // neuron migration // inferred from genetic interaction//0001934 // positive regulation of protein phos	
1219.1124	1655.5789	NM_019521		0.008	1.40	Gas6	growth arrest specific 6	0005576 // extracellular region // inferred from electronic annotation//0016020 // membrane // inferred from el	
146.06009	208.26578	NM_028608//XN_O		0.009	1.40	Glipr1	GLI pathogenesis-related 1 (glioma)	000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0	
343.43198	474.72325	NM_172154//XN_O		0.001	1.40	Lcor	ligand dependent nuclear receptor corepressor	0016020 // membrane // inferred from electronic annotation//0016021 // integral component of membrane // in	
408.04907	564.2121	NM_175518//XN_O		0.003	1.40	Tmem245	transmembrane protein 245	000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0006281 // Dt	
243.98155	339.63016	NM_001113333//NN		0.003	1.39	Cry2	cryptochrome 2 (photolyase-like)	0005515 // protein binding // inferred from electronic annotation//0017137 // Rab GTPase binding // not recorde	
329.148	455.91876	NM_172771//XN_O		0.009	1.39	Dmx12	Dmx-like 2	0006469 // negative regulation of protein kinase activity // not recorded//0032007 // negative regulation of TOR :	
240.03908	334.49823	NM_001037937//NN		0.007	1.39	Deptor	DEP domain containing MTOR-interacting protein	0006184 // GTP catabolic process // inferred from electronic annotation//0007165 // signal transduction // infern	
98.49426	144.27295	NM_001024474//XN		0.008	1.39	Diras2	DIRAS family, GTP-binding RAS-like 2	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006032 // chitin catabolic pr	
37.372078	54.18356	NM_007696		0.003	1.39	Ovgp1	oviductal glycoprotein 1	0007018 // microtubule-based movement // inferred from electronic annotation//0008152 // metabolic process /	
30.447065	43.374638	NM_001033170//XN		0.004	1.39	Fam83e	family with sequence similarity 83, member E	0005515 // protein binding // inferred from physical interaction	
165.02611	232.23625	NM_001109040//NN		0.010	1.39	Kif21a	kinesin family member 21A	0032747 // positive regulation of interleukin-23 production // not recorded//0071345 // cellular response to cyto	
210.46295	294.49002	NR_029468		0.001	1.39	Snhg12	small nucleolar RNA host gene 12	0032484 // Ral protein signal transduction // inferred from mutant phenotype//0032859 // activation of Ral GTPa	
158.4037	224.60265	NM_018828//XN_O		0.000	1.39	Fnbp4	formin binding protein 4	0001916 // positive regulation of T cell mediated cytotoxicity // not recorded//0002860 // positive regulation of n	
204.90239	286.09262	NM_008359//XN_O		0.001	1.38	Il17ra	interleukin 17 receptor A	0001541 // ovarian follicle development // inferred from mutant phenotype//0006351 // transcription, DNA-tem	
244.3725	337.89264	NM_001033348//XN		0.005	1.38	Ralgapa2	Ral GTPase activating protein, alpha subunit 2 (catalytic)	0006376 // mRNA splice site selection // inferred from electronic annotation//0006397 // mRNA processing // inf	
14.291265	19.655941	NM_001159424//NN		0.004	1.38	Il12a	interleukin 12a	0006281 // DNA repair // inferred from electronic annotation//0006351 // transcription, DNA-templated // infern	
497.98553	681.2343	NM_001290573//NN		0.002	1.38	Kmt2b	lysine (K)-specific methyltransferase 2B	0006085 // acetyl-CoA biosynthetic process // inferred from direct assay//0006085 // acetyl-CoA biosynthetic pro	
1064.6938	1431.9719	NM_026313//XN_O		0.002	1.38	Luc7l3//A1503301	LCUC-like 3 (S. cerevisiae)//expressed sequence A1503301	0003341 // cilium movement // inferred by curator//0006200 // ATP catabolic process // inferred from electronic	
695.4854	933.27936	NR_002845		0.008	1.38	Copg2os2	coatamer protein complex, subunit gamma 2, opposite strand 2	0006200 // ATP catabolic process // inferred from electronic annotation//0006810 // transport // inferred from el	
118.432434	169.44498	NM_001271962//NN		0.004	1.38	Eya2	eyes absent 2 homolog (Drosophila)	0001913 // T cell mediated cytotoxicity // ---//0002839 // positive regulation of immune response to tumor cell	
274.48474	375.48	NM_080575		0.003	1.37	Acs1	acyl-CoA synthetase short-chain family member 1	0007155 // cell adhesion // inferred from electronic annotation//0007420 // brain development // inferred from t	
3024.07	4055.1255	NM_030238		0.001	1.37	Dync1h1	dynein cytoplasmic 1 heavy chain 1	0001525 // angiogenesis // inferred from electronic annotation//0001568 // blood vessel development // inferrec	
360.7608	488.89444	NM_147219//XN_O		0.007	1.37	Abca5	ATP-binding cassette, sub-family A (ABC1), member 5	0000082 // G1/S transition of mitotic cell cycle // inferred from direct assay//0006281 // DNA repair // inferred fr	
20.263027	27.17836	NM_010400		0.004	1.37	H60a	histocompatibility 60a	0016021 // integral component of membrane // inferred from electronic annotation	
14.996394	20.318047	NM_001145977//NN		0.009	1.37	Cadm2	cell adhesion molecule 2	0006974 // cellular response to DNA damage stimulus // inferred from electronic annotation//0008152 // metabo	
1704.8632	2272.303	NM_001164564//NN		0.004	1.37	Egfl7	EGF-like domain 7	0030246 // carbohydrate binding // inferred from electronic annotation	
474.69678	642.2886	NM_016756//NM_1		0.004	1.37	Cdk2	cyclin-dependent kinase 2	000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0	
12.984719	17.603836	NM_001004182//XN		0.001	1.36	A930009E05RIK//Tmem178b	RIKEN cDNA A930009E05 gene//transmembrane protein 178B	0001122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenoty	
218.60852	299.85828	NM_001029856//XN		0.002	1.36	Atad5	ATPase family, AAA domain containing 5	0008152 // metabolic process // inferred from electronic annotation	
35.079273	49.494316	NM_133203//XN_O		0.005	1.36	Klra17	killer cell lectin-like receptor, subfamily A, member 17	0006897 // endocytosis // inferred from electronic annotation	
1136.2365	1499.445	NM_001012330//NN		0.002	1.36	Zbtb18	zinc finger and BTB domain containing 18	0006000 // fructose metabolic process // inferred from electronic annotation//0006003 // fructose 2,6-bisphosph	
1016.2122	1338.975	NM_001163215//NN		0.003	1.36	Fgfr3	fibroblast growth factor receptor 3	0006749 // glutathione metabolic process // inferred from sequence or structural similarity	
189.85846	261.89014	NM_178440//XN_O		0.002	1.36	Myo1g	myosin IG	000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from genetic interact	
51.388817	73.38285	NM_013825		0.006	1.36	Ly75	lymphocyte antigen 75	0006397 // mRNA processing // inferred from electronic annotation//0006468 // protein phosphorylation // infer	
77.229774	111.39694	NM_001162415//NN		0.007	1.36	Pfkfb2	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 2	0007155 // cell adhesion // inferred from electronic annotation//0005091 // leukocyte tethering or rolling // infer	
246.10506	333.69586	NM_153122//XN_O		0.002	1.36	Oplah	5-oxoprolinase (ATP-hydrolysing)	0001938 // positive regulation of endothelial cell proliferation // not recorded//0007275 // multicellular organis	
288.03516	388.91666	NM_144913//XN_O		0.001	1.36	Mepce	methylphosphate capping enzyme	0006629 // lipid metabolic process // inferred from electronic annotation//0006631 // fatty acid metabolic proces	
363.11362	488.96133	NM_013830//XN_O		0.001	1.36	Prpf4b	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	0006914 // autophagy // inferred from electronic annotation//0006915 // apoptotic process // inferred from elec	
275.38635	372.4274	NM_009151//XN_O		0.004	1.36	Selplg	SELP4 platelet (p-selectin) ligand	0002931 // response to ischemia // inferred from direct assay//0035235 // ionotropic glutamate receptor signalin	
198.40002	273.2777	NM_030168//XN_O		0.003	1.36	Rictor	RICTOR, independent companion of MTOR, complex 2	0006378 // mRNA polyadenylation // traceable author statement	
210.31165	288.02737	NM_007692//NM_0		0.009	1.36	Chkb//ChkbCpt1b//Cpt1b	choline kinase beta//Chkb-Cpt1b readthrough transcript (NMD candidate)//carnit	0000184 // nuclear-transcribed mRNA catabolic process, nonsense-mediated decay // not recorded//0006986 // i	
5232.082	6952.707	NM_027878//XN_O		0.003	1.35	Dram1	DNA-damage regulated autophagy modulator 1	0007010 // cytoskeleton organization // not recorded//0022604 // regulation of cell morphogenesis // not record	
846.0644	1117.9769	NM_001290676//NN		0.001	1.35	Cpeb4	cytoplasmic polyadenylation element binding protein 4	0006810 // transport // inferred from electronic annotation//0006812 // cation transport // inferred from electro	
18.109804	24.377796	NM_011033		0.002	1.35	Pabpc2	poly(A) binding protein, cytoplasmic 2	0000413 // protein peptidyl-prolyl isomerization // inferred from electronic annotation//0006457 // protein foldin	
662.10724	877.84503	NM_026573//XN_O		0.004	1.35	Upf3b	UPF3 regulator of nonsense transcripts homolog B (yeast)	0006810 // transport // inferred from electronic annotation	
178.81508	245.7998	NM_001099319//NN		0.001	1.35	Gm12942//Zmyhm6	predicted gene 12942//zinc finger, MYM-type 6	0006397 // mRNA processing // inferred from electronic annotation//0010923 // negative regulation of phosphat	
832.45593	1097.4224	NM_001038999//NN		0.002	1.35	Atp8a1	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenoty	
584.45013	775.4994	NM_011240		0.001	1.35	Ranbp2	RAN binding protein 2		
271.43558	365.693	NM_146013//XN_O		0.003	1.35	Sec14a	SEC14-like 4 (S. cerevisiae)		
216.18271	293.67044	NR_040628//NM_13		0.001	1.35	Gm17066//Rbm26	predicted gene 17066//RNA binding motif protein 26		
1014.3445	1326.374	NM_010207//NM_2		0.007	1.35	Fgfr2	fibroblast growth factor receptor 2		

[Nrf2-KO, Air, PBS]	[Nrf2-KO, Air, SFN]	RefSeq	Transcript ID	p	FC	PBS:SFN	Gene Symbol	Gene Title	Gene Ontology
472.12253	631.63904	NM_001288625	///NM	0.005	1.34		Arid3a	AT rich interactive domain 3A (BRIGHT-like)	0006351 // transcription, DNA-templated // inferred from electronic annotation
917.3113	1203.6443	NM_0011436	///NM	0.001	1.34		Sor1	soritin-related receptor, LDLR class A repeats-containing	0000042 // protein targeting to Golgi // not recorded
488.9552	653.52966	NM_001122675	///NM	0.001	1.34		Zcchc2	zinc finger, CCHC domain containing 2	0007154 // cell communication // inferred from electronic annotation
1314.8274	1714.4128	NM_010664	///XM_O	0.009	1.34		Krt18	keratin 18	0033209 // tumor necrosis factor-mediated signaling pathway // inferred from genetic interaction
433.61078	571.9356	NM_025845	///XM_O	0.004	1.33		Prpf38b	PRP38 pre-mRNA processing factor 38 (yeast) domain containing B	0006397 // mRNA processing // inferred from electronic annotation
298.26135	394.98712	NM_0011814	///NM	0.001	1.33		Fxr2	fragile X mental retardation, autosomal homolog 2	0003723 // RNA binding // inferred from electronic annotation
2606.6987	3370.1484	NM_001199136	///NM	0.001	1.33		Macf1	microtubule-actin crosslinking factor 1	0001707 // mesoderm formation // inferred from mutant phenotype
10575.217	13705.487	NM_011402	///XM_O	0.003	1.33		Slc34a2	solute carrier family 34 (sodium phosphate), member 2	0001701 // in utero embryonic development // inferred from mutant phenotype
35.97612	49.56613	NM_153529	///XM_O	0.008	1.33		Nrn1	neurtin 1	0007399 // nervous system development // not recorded
396.4879	520.0435			0.004	1.33		AK077428	Mus musculus 8 days embryo whole body cDNA, RIKEN full-length enriched library, clone:5730407P16 product:unclassifiable, full insert sequence.	
233.65855	311.17303	NM_001271587	///NM	0.002	1.33		Eps8	epidermal growth factor receptor pathway substrate 8	0008344 // adult locomotory behavior // inferred from mutant phenotype
301.84064	398.9988	NM_001165997	///NM	0.002	1.33		Spopl	speckle-type POZ protein-like	0016567 // protein ubiquitination // inferred from electronic annotation
609.439	790.1372	NM_001289690	///NM	0.004	1.33		Zfp740	zinc finger protein 740	0006351 // transcription, DNA-templated // inferred from electronic annotation
180.18382	242.82791	NM_009343	///XM_O	0.003	1.33		Phf1	PHD finger protein 1	0006351 // transcription, DNA-templated // inferred from electronic annotation
609.3109	791.4686	NM_134115	///XM_O	0.005	1.33		Stk38	serine/threonine kinase 38	0006464 // cellular protein modification process // not recorded
424.4299	556.1001	NM_011207	///XM_O	0.007	1.32		Ptpn3	protein tyrosine phosphatase, non-receptor type 3	0006470 // protein dephosphorylation // not recorded
197.18408	264.76764	NM_030014	///XM_O	0.003	1.32		Hook1	hook homolog 1 (Drosophila)	0006810 // transport // inferred from electronic annotation
376.61676	493.999	NM_001031814	///NM	0.002	1.32		Smg1	SMG1 homolog, phosphatidylinositol 3-kinase-related kinase (C. elegans)	0000184 // nuclear-transcribed mRNA catabolic process, nonsense-mediated decay // not recorded
688.90015	888.1753	NM_176836	///XM_O	0.006	1.32		Fam76b	family with sequence similarity 76, member B	0005634 // nucleus // not recorded
838.38586	1082.0266	NM_008551	///NM	0.002	1.32		Mapkapk2	MAP kinase-activated protein kinase 2	0002224 // toll-like receptor signaling pathway // inferred from mutant phenotype
332.17795	435.83673	NM_144916	///NM	0.007	1.32		Tmem150a	transmembrane protein 150A	0009056 // catabolic process // inferred from electronic annotation
200.45071	267.08893	NM_025806	///XM_O	0.010	1.32		Pibd1	phospholipase B domain containing 1	0006629 // lipid metabolic process // inferred from electronic annotation
585.27673	757.1203	NR_045008	///NM	0.005	1.32		Gm20300	predicted gene, 20300	
418.44238	546.31775	NM_019776	///XM_O	0.003	1.32		Snd1	staphylococcal nuclease and tudor domain containing 1	0001649 // osteoblast differentiation // not recorded
33.39544	45.240223	NM_170671	///XM_O	0.001	1.32		Mycbpap	MYCBP associated protein	0006897 // endocytosis // inferred from electronic annotation
28.863644	38.33517	NM_001293795	///NM	0.001	1.32		Tm6sf2	transmembrane 6 superfamily member 2	0016020 // membrane // inferred from electronic annotation
261.2709	342.62677	NM_001163766	///NM	0.003	1.31		Wdr90	WD repeat domain 90	0005515 // protein binding // inferred from electronic annotation
275.40002	361.2524	NM_001271358	///NM	0.004	1.31		Arrb2	arrestin, beta 2	0001932 // regulation of protein phosphorylation // inferred from direct assay
800.39984	1029.9666	NM_009427	///NM	0.004	1.31		Tob1	transducer of ErbB-2.1	0007184 // SMAD protein import into nucleus // inferred from direct assay
1727.8665	2195.1538	NM_176849	///XM_O	0.002	1.31		Arglu1	arginine and glutamate rich 1	0005515 // protein binding // inferred from electronic annotation
386.68106	502.51056	NM_001013414	///NM	0.009	1.31		Neurl4	neurallized homolog 4 (Drosophila)	0005737 // cytoplasm // inferred from electronic annotation
1565.5444	2000.6212	NM_001293667	///NM	0.003	1.31		Atp11a	ATPase, class VI, type 11A	0006810 // transport // inferred from electronic annotation
169.2596	226.04684	NM_001162945	///XA	0.004	1.31		Mtx3	metaxin 3	0006626 // protein targeting to mitochondrion // inferred from electronic annotation
39.551662	54.26534			0.005	1.31		Dnmbp	Mus musculus dynamin binding protein (Dnmbp), mRNA.	
383.36273	497.33185	NM_001081151	///NM	0.005	1.31		Gan	giant axonal neuropathy	0007010 // cytoskeleton organization // not recorded
23.972837	31.475975	NM_001042767	///NM	0.006	1.31		Proc	protein C	0006508 // proteolysis // inferred from direct assay
2014.5023	2557.106	NM_013605	///NM	0.005	1.31		Muc1	mucin 1, transmembrane	0001666 // response to hypoxia // inferred from electronic annotation
394.33856	510.55887	NM_001025307	///NM	0.005	1.31		Stx3	syntaxin 3	0006810 // transport // inferred from electronic annotation
439.56625	569.4507	NM_018824	///XM_O	0.005	1.30		Slc23a2	solute carrier family 23 (nucleobase transporters), member 2	0006810 // transport // inferred from electronic annotation
437.76752	566.42926	NM_153177	///XM_O	0.007	1.30		Ago4	argonaute RISC catalytic subunit 4	0006402 // mRNA catabolic process // not recorded
3274.0938	4193.465	NM_009864	///NM	0.006	1.30		Cdh1	cadherin 1	0001701 // in utero embryonic development // inferred from mutant phenotype
12.587478	16.356964	NM_007769	///XM_O	0.007	1.30		Dmbt1	deleted in malignant brain tumors 1	0001824 // blastocyst development // inferred from mutant phenotype
459.502	594.1198	NM_001197046	///NM	0.006	1.30		Gfgr1op	Fgfr1 oncogene partner	0006469 // negative regulation of protein kinase activity // not recorded
661.6627	842.575	NM_001025250	///NM	0.004	1.30		Vegfa	vascular endothelial growth factor A	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded
728.02295	924.3662	NM_172645	///XM_O	0.002	1.30		Suca	SUN domain containing ossification factor	0001503 // ossification // inferred from electronic annotation
265.25412	344.7731	NM_009201	///XM_O	0.003	1.30		Slc1a5	solute carrier family 1 (neutral amino acid transporter), member 5	0003333 // amino acid transmembrane transport // inferred from direct assay
346.88977	448.51886	NM_133921	///XM_O	0.008	1.30		Nfya1	nuclear transcription factor, X-box binding-like 1	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
37.38658	50.13584	NM_013486	///XM_O	0.006	1.30		Cd2	CD2 antigen	0007155 // cell adhesion // inferred from electronic annotation
1231.9764	1553.1554	NM_008986	///NM	0.008	1.30		Ptfr	polymerase I and transcript release factor	0006351 // transcription, DNA-templated // inferred from electronic annotation
516.6606	665.30255	NM_153056	///XM_O	0.003	1.30		Sirt7	sirtuin 7	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded
2233.261	2811.2349	NM_009170	///XM_O	0.002	1.30		Shh	sonic hedgehog	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay
278.69446	360.3511	NM_145151	///NR_O	0.004	1.30		Crebzf	CREB/ATF bZIP transcription factor	0006351 // transcription, DNA-templated // not recorded
139.60599	186.0955	NM_177372	///XR_38	0.005	1.29		Dna2	DNA replication helicase 2 homolog (yeast)	0000076 // DNA replication checkpoint // not recorded
3971.3213	5054.2412	NM_139149	///XM_O	0.003	1.29		Fus	fused in sarcoma	0000166 // nucleotide binding // inferred from electronic annotation
695.9025	879.6022	NM_019774	///XM_O	0.003	1.29		Akap8	A kinase (PRKA) anchor protein 8	0007076 // mitotic chromosome condensation // inferred from direct assay
233.93326	304.2318	NM_177806	///XM_O	0.008	1.29		Prpf39	PRP39 pre-mRNA processing factor 39 homolog (yeast)	0006396 // RNA processing // inferred from electronic annotation
470.99567	603.21295	NM_001005507	///NM	0.004	1.29		Smg7	Smg-7 homolog, nonsense mediated mRNA decay factor (C. elegans)	0000184 // nuclear-transcribed mRNA catabolic process, nonsense-mediated decay // inferred from electronic ann
730.8331	919.7546	NM_001160319	///NM	0.002	1.29		Ubr4	ubiquitin protein ligase E3 component n-recognin 4	0001657 // protein ubiquitination // inferred from electronic annotation
191.96724	251.37547	NM_146222	///XM_O	0.004	1.29		Msantd2	Myb/SANT-like DNA-binding domain containing 2	
648.00916	814.9779	NM_00115130	///NM	0.001	1.29		Zbtb44	zinc finger and BTB domain containing 44	
1493.5106	1867.6942	NM_001039581	///NM	0.003	1.28		Abca3	ATP-binding cassette, sub-family A (ABC1), member 3	
1055.8202	1326.7117	NM_001159963	///NM	0.002	1.28		Fbx15	F-box and leucine-rich repeat protein 5	
146.54016	193.85947	NM_207202	///NM	0.003	1.28		Cdc4120	coiled-coil domain containing 120	
2566.4402	3209.8403	NM_026499	///NM	0.004	1.28		Srsf6	serine/arginine-rich splicing factor 6	
74.15291	101.289955	NR_028380	///NR_O2	0.008	1.28		Ftx	Ftx transcript, Xist regulator (non-protein coding)	
1120.0303	1391.6128	NM_008532	///NM	0.003	1.28		Epcam	epithelial cell adhesion molecule	
903.1811	1124.0533	NM_173378	///NM	0.005	1.27		Tp53bp2	transformation related protein 53 binding protein 2	
534.7251	676.7039	NM_007651	///NM	0.006	1.27		Cd53	CD53 antigen	
167.33719	217.21092	NM_001168290	///NM	0.009	1.27		Supg2	SURP and G patch domain containing 2	
219.17746	281.06815	NM_178601	///XR_10	0.009	1.27		D1Ert448e	DNA segment, Chr 1, ERATO Doi 448, expressed	0006397 // mRNA processing // inferred from
1251.5516	1546.7518	NM_001034851	///NM	0.005	1.27		Fam134b	family with sequence similarity 134, member B	0006364 // rRNA processing // traceable author statement
								00019233 // sensory perception of pain // not recorded	

[Nrf2-KO, Air, PBS]	[Nrf2-KO, Air, SFN]	RefSeq	Transcript ID	p	FC	PBS:SFN	Gene Symbol	Gene Title	Gene Ontology
411.46655	516.79956	NM_001205353	///NM	0.003	1.27		Gramd4	GRAM domain containing 4	0006915 // apoptotic process // inferred from electronic annotation
608.4214	758.4442	NM_007462	///XM_O	0.009	1.27		Apc	adenomatosis polyposis coli	0000281 // mitotic cytokinesis // inferred from mutant phenotype//0000281 // mitotic cytokinesis // not recorded
565.25287	706.62305	NM_027349	///XM_O	0.005	1.27		Rbm25	RNA binding motif protein 25	0000381 // regulation of alternative mRNA splicing, via spliceosome // inferred from electronic annotation//0000381 // regulation of alternative mRNA splicing, via spliceosome
399.18823	500.93253	NM_153790	///XM_O	0.006	1.27		Scarf2	scavenger receptor class F, member 2	0006898 // receptor-mediated endocytosis // inferred from direct assay//0007155 // cell adhesion // inferred from
2450.2734	3027.0522	NM_001145824	///NM	0.005	1.27		Hipk3	homeodomain interacting protein kinase 3	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from sequence or str
1519.6454	1867.6646	NM_008149	///XM_O	0.005	1.27		Gpam	glycerol-3-phosphate acyltransferase, mitochondrial	0006629 // lipid metabolic process // inferred from electronic annotation//0006631 // fatty acid metabolic proces
518.90076	652.2919	NM_001081171	///XM	0.006	1.27		Lama5	laminin, alpha 5	0001658 // branching involved in ureteric bud morphogenesis // inferred from mutant phenotype//0001738 // m
746.5401	925.05383	NM_001081039	///NM	0.005	1.26		Dock9	dedicator of cytokinesis 9	0007264 // small GTPase mediated signal transduction // inferred from electronic annotation//0032319 // regulat
24.511972	31.13356	NM_001281955	///XM	0.005	1.26		Csmd2	CUB and Sushi multiple domains 2	
535.93176	671.21704	NM_001081150		0.006	1.26		Lonrf1	LON peptidase N-terminal domain and ring finger 1	0006200 // ATP catabolic process // inferred from electronic annotation//0006508 // proteolysis // inferred from
704.786	870.77216	NM_144925	///XM_O	0.010	1.26		Tnrc6a	trinucleotide repeat containing 6a	0006417 // regulation of translation // inferred from electronic annotation//0009267 // cellular response to starv.
412.89673	516.568	NM_001045523	///XM	0.010	1.26		Bahd1	bromo adjacent homology domain containing 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcr
4610.6074	5672.172	NM_001081286	///XM	0.003	1.26		Fat1	FAT tumor suppressor homolog 1 (Drosophila)	0007015 // actin filament organization // inferred from mutant phenotype//0007155 // cell adhesion // inferred f
1721.9828	2111.8345	NM_001025387	///NM	0.010	1.26		Brd2	bromodomain containing 2	0006334 // nucleosome assembly // not recorded//0006351 // transcription, DNA-templated // inferred from elec
204.48326	260.37762	NM_001136088	///NM	0.008	1.26		Sh3bp2	SH3-domain binding protein 2	0005515 // protein binding // inferred from physical interaction//0005543 // phospholipid binding // inferred fror
395.9646	493.76358	NM_001045529	///XM	0.008	1.26		Morc3	microchidia 3	0006468 // protein phosphorylation // not recorded//0007569 // cell aging // not recorded//0009791 // post-en
580.33966	720.61646	NM_0018759	///NR_O	0.002	1.26		Zfp326	zinc finger protein 326	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcr
418.92673	522.90533	NM_133829	///NM_1	0.009	1.26		Mfsd6	major facilitator superfamily domain containing 6	0002376 // immune system process // inferred from electronic annotation//0055085 // transmembrane transport
587.98303	728.3994	NM_001145813	///NM	0.009	1.26		Elf5	E74-like factor 5	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcr
138.86198	181.14723	NM_133770	///XM_O	0.003	1.26		Adck4	aarF domain containing kinase 4	0006468 // protein phosphorylation // inferred from electronic annotation//0008152 // metabolic process // infe
280.98007	352.43027	NM_001164184	///NM	0.004	1.26		Lsr	lipolysis stimulated lipoprotein receptor	0001889 // liver development // inferred from mutant phenotype//0006898 // receptor-mediated endocytosis //
487.2165	607.7341	NM_017463		0.004	1.26		Pbx2	pre B cell leukemia homeobox 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcr
667.5678	820.72095	NM_001285870	///NM	0.008	1.26		Trim3	tripartite motif-containing 3	0006810 // transport // inferred from electronic annotation//0015031 // protein transport // inferred from electr
1311.7941	1596.239	NM_001287180	///NM	0.006	1.26		Atf4	activating transcription factor 4	0006094 // gluconeogenesis // inferred from direct assay//0006351 // transcription, DNA-templated // inferred fr
329.62616	411.33902	NM_080553	///XM_O	0.004	1.25		Itp3	inositol 1,4,5-triphosphate receptor 3	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic
382.41815	478.77054	NM_001166648	///NM	0.008	1.25		Zfp280c	zinc finger protein 280C	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcr
1088.8774	1335.6722	NM_001217599	///NM	0.009	1.25		Sort1	sortilin 1	0001503 // ossification // inferred from electronic annotation//0006810 // transport // inferred from electronic a
500.95636	622.4535	NM_001146176	///NM	0.010	1.25		Max	Max protein	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcr
233.95839	295.29355	NM_026888	///XM_O	0.005	1.25		Phkg2	phosphorylase kinase, gamma 2 (testis)	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0005977 // glycogen metabol
356.93933	445.84897	NM_001081049	///XM	0.003	1.25		Kmt2a	lysine (K)-specific methyltransferase 2A	0006306 // DNA methylation // inferred from mutant phenotype//0006351 // transcription, DNA-templated // inf
731.56586	895.31793	NM_010690	///XM_O	0.009	1.25		Lats1	large tumor suppressor	0000086 // G2/M transition of mitotic cell cycle // not recorded//0000819 // sister chromatid segregation // not r
380.66827	473.32748	NM_172652	///XM_O	0.004	1.25		Kansl3	KAT8 regulatory NSL complex subunit 3	0016568 // chromatin modification // inferred from electronic annotation//0043981 // histone H4-K5 acetylation
626.3747	766.0071	NM_144837	///XM_O	0.008	1.25		Ice1	interactor of little elongation complex ELL subunit 1	
727.53564	891.14105	NM_172866	///XM_O	0.003	1.25		Rgp1	RGP1 retrograde golgi transport homolog (S. cerevisiae)	
1297.6232	1574.0868	NM_177301	///XM_O	0.006	1.25		Hnrnp1	heterogeneous nuclear ribonucleoprotein L	0006397 // mRNA processing // inferred from electronic annotation
1788.1697	2166.5437	NM_011519	///XM_O	0.004	1.25		Sdc1	syndecan 1	0001657 // ureteric bud development // inferred from electronic annotation//0006954 // inflammatory response
205.466	259.38693	NM_009886	///XM_O	0.008	1.25		Celsr1	cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, Drosophila)	0001702 // gastrulation with mouth forming second // non-traceable author statement//0001736 // establishmer
321.0384	396.3768	NM_009461	///XM_O	0.004	1.24		Ubr1	ubiquitin protein ligase E3 component n-recogin 1	0006511 // ubiquitin-dependent protein catabolic process // inferred from direct assay//0006511 // ubiquitin-dep
1534.4547	1861.2865	NM_178920		0.006	1.24		Mal2	mal, T cell differentiation protein 2	0005515 // protein binding // inferred from electronic annotation
254.1309	316.2108	NM_023229	///XM_O	0.010	1.24		Fastk	Fas-activated serine/threonine kinase	0006468 // protein phosphorylation // not recorded//0006915 // apoptotic process // inferred from electronic an
264.01752	328.5755	NM_001253752	///NM	0.004	1.24		Zmym5	zinc finger, MYM-type 5	0008270 // zinc ion binding // inferred from electronic annotation//0046872 // metal ion binding // inferred from
810.8788	977.0885	NM_010585	///XM_O	0.006	1.24		Itp1	inositol 1,4,5-trisphosphate receptor 1	0001666 // response to hypoxia // inferred from direct assay//0001666 // response to hypoxia // not recorded//
506.74896	623.7485	NM_029868	///XM_O	0.008	1.24		Gpbp11	GC-rich promoter binding protein 1-like 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcr
399.1241	491.10736	NM_001290783	///NM	0.006	1.24		Wdr13	WD repeat domain 13	0005515 // protein binding // inferred from electronic annotation
296.8177	365.09445	NM_001289429	///NM	0.007	1.23		Cipc	CLOCK interacting protein, circadian	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcr
345.6085	423.71396	NM_201362	///XM_O	0.008	1.23		Ccdc68	coiled-coil domain containing 68	
3586.9675	4410.366	NM_007569		0.008	1.23		Btg1	B cell translocation gene 1, anti-proliferative	0006479 // protein methylation // inferred from direct assay//0006979 // response to oxidative stress // inferred
91.4678	119.54797	NM_001163749	///NM	0.006	1.23		Camsap3	calmodulin regulated spectrin-associated protein family, member 3	0000226 // microtubule cytoskeleton organization // not recorded//0010923 // negative regulation of phosphata:
1254.9084	1502.8506	NM_001164503	///XM	0.010	1.23		Akap11	A kinase (PRKA) anchor protein 11	0010738 // regulation of protein kinase A signaling // not recorded//0042325 // regulation of phosphorylation // i
411.1055	502.8651	NM_133757	///XM_O	0.009	1.23		Pgs1	phosphatidylglycerophosphate synthase 1	0006629 // lipid metabolic process // inferred from electronic annotation//0006655 // phosphatidylglycerol biosy
541.69824	660.2406	NM_001173547	///NM	0.008	1.23		Taz	tafazzin	0006936 // muscle contraction // not recorded//0007507 // heart development // not recorded//0007519 // ske
317.12598	388.85678	NM_198170	///XM_O	0.009	1.23		Szt2	seizure threshold 2	0007417 // central nervous system development // inferred from mutant phenotype//0009790 // embryo develop
1376.9081	1637.7526	NM_021604	///XM_O	0.010	1.23		Agrn	agrin	0001932 // regulation of protein phosphorylation // not recorded//0001934 // positive regulation of protein phos
213.4828	264.86884	NM_028047	///XM_O	0.010	1.23		Smg9	smg-9 homolog, nonsense mediated mRNA decay factor (C. elegans)	0000184 // nuclear-transcribed mRNA catabolic process, nonsense-mediated decay // not recorded
409.05075	497.6229	NM_018748	///XM_O	0.008	1.22		Golga4	golgi autoantigen, golgin subfamily a, 4	0000042 // protein targeting to Golgi // inferred from electronic annotation//0006355 // regulation of transcripti
2219.8306	2625.3403	NM_001146120	///NM	0.007	1.22		Psp	prosaposin	0006629 // lipid metabolic process // inferred from electronic annotation//0006665 // sphingolipid metabolic pro
927.72565	1105.54	NM_001040459	///XM	0.006	1.22		Shroom4	shroom family member 4	0000902 // cell morphogenesis // inferred from sequence or structural similarity//0007015 // actin filament orga
6579.4795	7937.7295	NM_001171034	///NM	0.009	1.22		Tmbim6	transmembrane BAX inhibitor motif containing 6	0006915 // apoptotic process // inferred from electronic annotation//0006986 // response to unfolded protein //
740.0734	880.781	NM_009796	///XM_O	0.009	1.22		Capn7	calpain 7	0006508 // proteolysis // not recorded//0010634 // positive regulation of epithelial cell migration // not recorded
830.67487	984.8433	NM_001276292	///NM	0.008	1.22		Wwp1	WW domain containing E3 ubiquitin protein ligase 1	0016567 // protein ubiquitination // inferred from direct assay//0016567 // protein ubiquitination // traceable au
18.76382	22.56707	NM_146086	///XM_O	0.006	1.21		Pde6a	phosphodiesterase 6A, cGMP-specific, rod, alpha	0007165 // signal transduction // inferred from electronic annotation//0007601 // visual perception // inferred fr
1052.1464	1251.0677	NM_025611		0.009	1.21		Cul7	culin 7	0000226 // microtubule cytoskeleton organization // inferred from sequence or structural similarity//0000281 // i
918.99493	1085.121	NM_001290792	///NM	0.007	1.21		Wdr45	WD repeat domain 45	0000045 // autophagic vacuole assembly // not recorded//0006914 // autophagy // not recorded//0050790 // r
2174.6592	2561.4438	NM_144900		0.010	1.21		Atp1a1	ATPase, Na+/K+ transporting, alpha 1 polypeptide	0002026 // regulation of the force of heart contraction // inferred from mutant phenotype//0002028 // regulatio
2213.297	2597.9736	NM_206924		0.009	1.21		Jtb	jumping translocation breakpoint	0000910 // cytokinesis // not recorded//0006915 // apoptotic process // inferred from electronic annotation//00
232.40111	282.9332	NM_001170433	///NM	0.007	1.21		Ppfjbp1	PTPRF interacting protein, binding protein 1 (liprin beta 1)	0005515 // protein binding // inferred from electronic annotation
523.5016	627.2216	NM_001165894	///NM	0.006	1.21		Akt1	thymoma viral proto-oncogene 1	0000060 // protein import into nucleus, translocation // not recorded//0001649 // osteoblast differentiation // in
342.91522	411.1354	NM_001253885	///NM	0.009	1.21		Apbb1	amyloid beta (A4) precursor protein-binding, family B, member 1	0001764 // neuron migration // inferred from genetic interaction//0006302 // double-strand break repair // infer
931.9625	1098.9344	NM_011682	///XM_O	0.007	1.21		Utrn	utrophin	0001954 // positive regulation of cell-matrix adhesion // not recorded//0007527 // adult somatic muscle develop
694.9422	819.30725	NM_001252326	///NM	0.010	1.21		Pan2	PAN2 polyA specific ribonuclease subunit homolog (S. cerevisiae)	0000184 // nuclear-transcribed mRNA catabolic process, nonsense-mediated decay // inferred from electronic ann
76.91728	68.19983	NM_029182		0.008	-1.19		Rasd2	RASD family, member 2	0001963 // synaptic transmission, dopaminergic // inferred from mutant phenotype//0006184 // GTP catabolic pr

[Nrf2-KO, Air, PBS]	[Nrf2-KO, Air, SFN]	RefSeq	Transcript ID	p	FC	PBS:SFN	Gene Symbol	Gene Title	Gene Ontology
11392.251	9199.467	NM_001077529///NM		0.009	-1.20		Nme2	NME/NM23 nucleoside diphosphate kinase 2	0002762 // negative regulation of myeloid leukocyte differentiation // not recorded///0006165 // nucleoside diphosphate kinase activity
1646.1176	1348.7761	NM_001161724///NM		0.010	-1.20		Ilk	integrin linked kinase	0001558 // regulation of cell growth // not recorded///0001658 // branching involved in ureteric bud morphogenesis
205.99272	177.18608	NM_001042556///NM		0.009	-1.20		Rpf2	ribosome production factor 2 homolog (S. cerevisiae)	0044822 // poly(A) RNA binding // not recorded
125.604965	111.07297	NM_029101///XR_38		0.008	-1.20		Rrp7a	ribosomal RNA processing 7 homolog A (S. cerevisiae)	0000166 // nucleotide binding // inferred from electronic annotation///0003723 // RNA binding // inferred from electronic annotation
48.495747	41.14084	NM_008024		0.007	-1.21		Foxl1	forkhead box L1	0000122 // negative regulation of transcription from RNA polymerase II promoter // --///0006351 // transcription, DNA-templated
405.3909	335.4976	NM_026062		0.009	-1.21		Fam69a	family with sequence similarity 69, member A	0005515 // protein binding // inferred from physical interaction
569.2749	467.8062	NM_001024384///NM		0.008	-1.21		Crfs1	cardiolipin synthase 1	0006629 // lipid metabolic process // inferred from electronic annotation///0008654 // phospholipid biosynthetic process
421.15665	348.99915	NM_153160///XM_0		0.010	-1.21		Zcchc17	zinc finger, CCHC domain containing 17	0003676 // nucleic acid binding // inferred from electronic annotation///0003723 // RNA binding // traceable author statement
238.09058	201.72334	NM_001127338///NM		0.008	-1.21		Aldh7a1	aldehyde dehydrogenase family 7, member A1	0008152 // metabolic process // inferred from electronic annotation///0019285 // glycine betaine biosynthetic process
112.27865	98.583206	NM_027201///XM_0		0.010	-1.21		Zfp511	zinc finger protein 511	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-templated
119.83843	104.907814	NM_138649///XM_0		0.007	-1.21		Syt17	synaptotagmin XVII	0006810 // transport // inferred from electronic annotation///0006887 // exocytosis // inferred from electronic annotation
73.42475	63.656742	NM_001044386///NM		0.009	-1.22		Zfp-ps1///Zfx	zinc finger protein, autosomal, pseudogene//zinc finger protein X-linked	0001541 // ovarian follicle development // inferred from mutant phenotype///0006351 // transcription, DNA-templated
117.91455	103.2395	NM_001276442///NM		0.010	-1.22		Acy1	aminoacylase 1	0006508 // proteolysis // inferred from electronic annotation///0006520 // cellular amino acid metabolic process
60.109657	51.34152	NM_010827///XM_0		0.009	-1.22		Msc	musculin	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0007155 // cell adhesion // inferred from electronic annotation///0008360 // regulation of cell shape // inferred from electronic annotation
1380.3821	1116.8933	NM_001163256///NM		0.009	-1.22		Fblim1	filamin binding LIM protein 1	
277.51715	230.42418	NM_001134902///NM		0.007	-1.22		AU019823	expressed sequence AU019823	
2221.04	1777.0048	NM_011967		0.007	-1.22		Pasma5	proteasome (prosome, macropain) subunit, alpha type 5	0006508 // proteolysis // inferred from electronic annotation///0006511 // ubiquitin-dependent protein catabolic process
16.359215	13.376959	NM_011272		0.008	-1.22		Rln1	relaxin 1	0007188 // adenylate cyclase-modulating G-protein coupled receptor signaling pathway // not recorded///001074
291.30392	241.39128	NM_001085508///XM		0.006	-1.22		Tmem8b	transmembrane protein 88	0007155 // cell adhesion // inferred from electronic annotation///0007160 // cell-matrix adhesion // not recorded, traceable author statement
515.34766	421.1316	NM_001080742///NM		0.007	-1.22		Vamp5	vesicle-associated membrane protein 5	0006887 // exocytosis // not recorded///0006906 // vesicle fusion // not recorded///0007269 // neurotransmitter release
890.584	719.23444	NM_024282///XM_0		0.005	-1.22		Desi2	desmoylating isopeptidase 2	0006508 // proteolysis // inferred from electronic annotation
146.01375	126.43931	NM_001014395///XM		0.008	-1.22		Fbxw22	F-box and WD-40 domain protein 22	0005515 // protein binding // inferred from electronic annotation
265.46164	220.79482	NM_001163239///NM		0.008	-1.22		Nqo2	NAD(P)H dehydrogenase, quinone 2	0007613 // memory // inferred from electronic annotation///0005514 // oxidation-reduction process // inferred from electronic annotation
65.82909	56.313026	NM_001033312///XM		0.005	-1.22		Fbxl18	F-box and leucine-rich repeat protein 18	0005515 // protein binding // inferred from electronic annotation
307.13614	253.10446	NM_011785///XM_0		0.010	-1.22		Akt3	thymoma viral proto-oncogene 3	0000002 // mitochondrial genome maintenance // not recorded///0006468 // protein phosphorylation // not recorded
989.39264	794.8956	NM_008723///NR_OC		0.006	-1.23		Npm3///Npm3-ps1	nucleoplasm 3//nucleoplasm 3, pseudogene 1	0006364 // rRNA processing // inferred from direct assay///0009303 // rRNA transcription // inferred from electronic annotation
989.39264	794.8956	NM_008723///NR_OC		0.006	-1.23		Npm3///Npm3-ps1	nucleoplasm 3//nucleoplasm 3, pseudogene 1	0006364 // rRNA processing // inferred from direct assay///0009303 // rRNA transcription // inferred from direct assay
539.2666	438.72354	NM_019432		0.006	-1.23		Tmem37	transmembrane protein 37	0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from electronic annotation
21.371939	17.196777	NR_045047		0.006	-1.23		Tunar	Tcl1 upstream neural differentiation associated RNA	
879.75104	706.1113	NM_015792///XM_0		0.007	-1.23		Fbxo18	F-box protein 18	0008152 // metabolic process // inferred from electronic annotation///00032508 // DNA duplex unwinding // inferred from electronic annotation
192.7467	163.50467	NM_207298///XM_0		0.010	-1.23		Cercam	cerebral endothelial cell adhesion molecule	0007155 // cell adhesion // not recorded///0009103 // lipopolysaccharide biosynthetic process // inferred from electronic annotation
453.47842	368.91324	NM_127575///NM_1		0.008	-1.23		Zfp277	zinc finger protein 277	0007301 // cellular response to hydrogen peroxide // inferred from mutant phenotype///2000772 // regulation of transcription, DNA-templated
117.295425	101.215195	NM_148938		0.004	-1.23		Slc1a3	solute carrier family 1 (glial high affinity glutamate transporter), member 3	0006536 // glutamate metabolic process // inferred from mutant phenotype///0006537 // glutamate biosynthetic process
622.91656	501.30685	NM_009148///XM_0		0.010	-1.23		Exoc4	exocyst complex component 4	0006612 // protein targeting to membrane // not recorded///0006810 // transport // inferred from electronic annotation
43.16491	35.877193	XR_105083///XR_107		0.009	-1.23		Gm12758	predicted gene 12758	
174.06857	148.93547	NM_001159331///NM		0.005	-1.23		N6amt1	N-6 adenine-specific DNA methyltransferase 1 (putative)	0006479 // protein methylation // not recorded///0030307 // positive regulation of cell growth // not recorded///0005515 // protein binding // inferred from electronic annotation
157.58698	135.20943	NM_127945///XM_0		0.006	-1.23		Ankrd13b	ankyrin repeat domain 13b	0006810 // transport // inferred from electronic annotation///0006886 // intracellular protein transport // inferred from electronic annotation
929.68524	743.5187	NM_011591///XM_0		0.006	-1.23		Timm17b	translocase of inner mitochondrial membrane 17b	0010193 // response to ozone // inferred from electronic annotation///0010477 // response to sulfur dioxide // inferred from electronic annotation
95.04872	81.67747	NM_010844///XM_0		0.009	-1.23		Muc5ac	mucin 5, subtypes A and C, tracheobronchial/gastric	0002098 // tRNA wobble uridine modification // not recorded///0002143 // tRNA wobble position uridine thiolation
86.94642	74.40261	NM_001160330		0.010	-1.24		Mocs3	molybdenum cofactor synthesis 3	0006508 // proteolysis // inferred from electronic annotation///0010243 // response to organonitrogen compound
2443.5093	1936.4417	NM_011970///XM_0		0.008	-1.24		Psmb2	proteasome (prosome, macropain) subunit, beta type 2	0008152 // metabolic process // inferred from electronic annotation
493.4236	397.2164	NM_025798///XM_0		0.007	-1.24		Hint3	histidine triad nucleotide binding protein 3	0006812 // cation transport // not recorded///0006821 // chloride transport // not recorded///1902476 // chloride ion transport
351.0264	285.8242	NM_001271873///NM		0.005	-1.24		Ano10	anoctamin 10	0006508 // proteolysis // inferred from electronic annotation///0051603 // proteolysis involved in cellular protein catabolic process
1409.6046	1121.9183	NM_011185		0.007	-1.24		Psmb1	proteasome (prosome, macropain) subunit, beta type 1	0007165 // signal transduction // inferred from electronic annotation///0007601 // visual perception // inferred from electronic annotation
55.610065	46.34353	NM_008189		0.008	-1.24		Guca1a	guanylate cyclase activator 1a (retina)	0006184 // GTP catabolic process // inferred from electronic annotation///0007165 // signal transduction // inferred from electronic annotation
255.35707	211.1263	NM_025931		0.007	-1.24		Ifi271	intraflagellar transport 27	0006412 // translation // inferred from direct assay///0006412 // translation // not recorded///0006413 // translation
1503.741	1198.7594	NM_026114		0.010	-1.24		Eif2s1	eukaryotic translation initiation factor 2, subunit 1 alpha	0000165 // MAPK cascade // inferred from electronic annotation///0000186 // activation of MAPKK activity // inferred from electronic annotation
158.36768	135.47089	NM_001081292///NM		0.009	-1.24		Map3k10	mitogen-activated protein kinase kinase 10	0007165 // signal transduction // inferred from electronic annotation
49.822277	40.91523	NM_028474///XM_0		0.006	-1.24		Ptchd4	patched domain containing 4	0001755 // neural crest cell migration // not recorded///0007169 // transmembrane receptor protein tyrosine kinase activity
266.6047	220.19589	NM_008738///XM_0		0.008	-1.24		Nrtn	neurturin	0000212 // meiotic spindle organization // inferred from expression pattern///0006184 // GTP catabolic process // inferred from electronic annotation
410.37567	332.3897	NM_134024		0.005	-1.24		Tubg1	tubulin, gamma 1	0006508 // proteolysis // not recorded///0030163 // protein catalytic process // traceable author statement///0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-templated
2634.9792	2072.5742	NM_011971		0.009	-1.24		Psmb3	proteasome (prosome, macropain) subunit, beta type 3	0006506 // GPI anchor biosynthetic process // not recorded///0009893 // positive regulation of metabolic process
123.25133	105.12771	NM_007922		0.010	-1.24		Elk1	ELK1, member of ETS oncogene family	0022011 // myelination in peripheral nervous system // not recorded///0032319 // regulation of Rho GTPase activity
787.7596	625.82385	NM_025574		0.010	-1.24		Pyrj	Pigj upstream reading frame	
137.68909	117.15027	NM_001037736///NM		0.005	-1.24		Arhgef10	Rho guanine nucleotide exchange factor (GEF) 10	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-templated
46.323574	37.967438	XR_376884///XR_376		0.006	-1.24		2210406O10Rik	RIKEN cDNA 2210406O10 gene	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-templated
24.71157	19.674719	NM_029416///XM_0		0.007	-1.24		Klf17	Kruppel-like factor 17	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-templated
649.7859	516.76373	NM_001177945///NM		0.005	-1.24		Aamdac	adipogenesis associated Mth938 domain containing	0043066 // negative regulation of apoptotic process // inferred from mutant phenotype///0045600 // positive regulation of cell growth
232.44029	192.35313	NM_001033314///XM		0.003	-1.25		Ccdc61	coiled-coil domain containing 61	0005813 // centrosome // not recorded
989.9023	783.88446	NM_029354///XM_0		0.004	-1.25		Mzt2	mitotic spindle organizing protein 2	0005737 // cytoplasm // inferred from electronic annotation///0005813 // centrosome // not recorded///0005815 // cytoskeleton organization
101.54686	86.47637	NM_001294308///NM		0.008	-1.25		Ngb	neuroglobin	0006810 // transport // inferred from electronic annotation///0006915 // apoptotic process // inferred from electronic annotation
612.22876	488.40732	NM_001164212///NM		0.009	-1.25		Rerg	RAS-like, estrogen-regulated, growth-inhibitor	0006184 // GTP catabolic process // not recorded///0007165 // signal transduction // inferred from electronic annotation
384.34775	310.46234	NM_026113///XM_0		0.006	-1.25		Gtf3c6	general transcription factor IIIC, polypeptide 6, alpha	0006351 // transcription, DNA-templated // not recorded///0006383 // transcription from RNA polymerase III promoter
234.521	193.99869	NM_026015///XM_0		0.008	-1.25		Zmat5	zinc finger, matrix type 5	0006397 // mRNA processing // inferred from electronic annotation///0008380 // RNA splicing // inferred from electronic annotation
470.45953	377.14816	NM_021428///XM_0		0.007	-1.25		Dexi	dexamethasone-induced transcript	
46.05425	37.707077	NM_001122639///NM		0.008	-1.25		Galnt9	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 9	0006486 // protein glycosylation // inferred from electronic annotation///0008152 // metabolic process // inferred from electronic annotation
66.13625	55.53621	NM_028411///XM_0		0.007	-1.25		Tmem138	transmembrane protein 138	0030030 // cell projection organization // inferred from electronic annotation///0042384 // cilium assembly // not recorded
39.58425	32.221634	NM_001080934///XM		0.009	-1.25		Slc16a5	solute carrier family 16 (monocarboxylic acid transporters), member 5	0006810 // transport // inferred from electronic annotation///0055085 // transmembrane transport // inferred from electronic annotation
720.2045	570.7497	NM_025375///XM_0		0.006	-1.25		Wbscr22	Williams Beuren syndrome chromosome region 22	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-templated
163.35278	138.26282	NM_001254762///NM		0.007	-1.25		Mospd3	motile sperm domain containing 3	0007507 // heart development // inferred from mutant phenotype
156.05014	131.78233	NM_009088///XM_0		0.008	-1.25		Poir1a	polymerase (RNA) I polypeptide A	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006360 // transcription from RNA polymerase II promoter

[Nrf2-KO, Air, PBS]	[Nrf2-KO, Air, SFN]	RefSeq	Transcript ID	p	FC	PBS:SFN	Gene Symbol	Gene Title	Gene Ontology
535.29517	425.36746	NM_001162521	///NM	0.005	-1.25		<i>Dguak</i>	deoxyguanosine kinase	0006139 // nucleobase-containing compound metabolic process // traceable author statement///0006468 // prote
26.434654	20.879622	NM_001007573	///XA	0.006	-1.25		<i>Maneal</i>	mannosidase, endo-alpha-like	0008152 // metabolic process // inferred from electronic annotation
1734.5222	1356.5464	NM_019953	///XM_OI	0.005	-1.25		<i>Cnpy2</i>	canopy 2 homolog (zebrafish)	0010629 // negative regulation of gene expression // inferred from mutant phenotype///0010988 // regulation of
162.99133	137.81621	NM_001081179	///NM	0.006	-1.25		<i>Heatr5b</i>	HEAT repeat containing 5B	0005488 // binding // inferred from electronic annotation///0005515 // protein binding // inferred from physical i
1230.6725	963.49365	NM_001261	///NM	0.006	-1.26		<i>Fundc2</i>	FUN14 domain containing 2	0005634 // nucleus // not recorded///0005739 // mitochondrion // not recorded
230.83437	189.71242	NM_172522	///XM_OI	0.007	-1.26		<i>Mrpl21</i>	mitochondrial ribosomal protein L21	0006412 // translation // inferred from electronic annotation
284.14886	229.68207	NM_0025525	///NM	0.003	-1.26		<i>Rnf113a2</i>	ring finger protein 113A2	0005515 // protein binding // inferred from electronic annotation///0008270 // zinc ion binding // inferred from el
1228.8027	963.52545	NM_013902	///NM	0.003	-1.26		<i>Fkbp3</i>	FK506 binding protein 3	0000413 // protein peptidyl-prolyl isomerization // not recorded///0006457 // protein folding // inferred from elec
558.4193	442.84793	NM_026230	///NM_2	0.009	-1.26		<i>H2afy2</i> /// <i>H2afy3</i>	H2A histone family, member Y2///H2A histone family, member Y3	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded///0006334 // nu
65.65393	54.662155	NM_008593	///NM	0.009	-1.26		<i>Foxd2</i>	forkhead box D2	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded///0001658 // br
449.9475	357.03183	NM_029632	///NM	0.005	-1.26		<i>Ppp1r11</i>	protein phosphatase 1, regulatory (inhibitor) subunit 11	0043086 // negative regulation of catalytic activity // inferred from direct assay
33.219917	26.500816	NM_009890	///NM	0.010	-1.26		<i>Ch25h</i>	cholesterol 25-hydroxylase	0006629 // lipid metabolic process // inferred from electronic annotation///0006633 // fatty acid biosynthetic pro
348.38257	278.60934	NM_001285899	///NM	0.005	-1.26		<i>Eri3</i>	exoribonuclease 3	0008152 // metabolic process // inferred from electronic annotation///0090305 // nucleic acid phosphodiester bo
98.80254	83.39764	NM_001113211	///NM	0.010	-1.26		<i>1700012D01Rik</i> /// <i>Tmem194</i>	RIKEN cDNA 1700012D01 gene///transmembrane protein 194	0016020 // membrane // inferred from electronic annotation///0016021 // integral component of membrane // in
64.66186	53.546825	NM_023695	///XM_OI	0.006	-1.26		<i>Crybb1</i>	crystallin, beta B1	0005212 // structural constituent of eye lens // not recorded///0005515 // protein binding // inferred from physi
2929.6816	2277.4053	NM_025511	///NM	0.008	-1.26		<i>Cox20</i>	COX20 Cox2 chaperone	0005739 // mitochondrion // inferred from direct assay///0005739 // mitochondrion // not recorded///0016020 // in
39.658686	31.834368	NM_008622	///NM	0.003	-1.26		<i>Onecut1</i>	one cut domain, family member 1	0001889 // liver development // inferred from genetic interaction///0001952 // regulation of cell-matrix adhesion
187.26993	155.51958	NM_023556	///XM_OI	0.007	-1.26		<i>Mvk</i>	mevalonate kinase	0006629 // lipid metabolic process // inferred from electronic annotation///0006694 // steroid biosynthetic proces
764.88684	598.97253	NM_023587	///XM_OI	0.003	-1.26		<i>Ptp1b</i>	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b	0006629 // lipid metabolic process // inferred from electronic annotation///0006631 // fatty acid metabolic proces
1018.7957	799.08026	NM_011895	///XM_OI	0.006	-1.26		<i>Slc35a1</i>	solute carrier family 35 (CMP-sialic acid transporter), member 1	0006810 // transport // inferred from electronic annotation///0008643 // carbohydrate transport // inferred from
24.682493	19.322618	NM_001099631	///NM	0.003	-1.26		<i>Sh2d5</i>	SH2 domain containing 5	0005515 // protein binding // inferred from electronic annotation
296.38144	238.13055	NM_001163170	///NM	0.006	-1.26		<i>Lix1l</i>	Lix1-like	0005515 // protein binding // inferred from electronic annotation
415.78082	330.5474	NM_001122960	///NM	0.005	-1.26		<i>Cdc53</i>	coiled-coil domain containing 53	0016020 // membrane // inferred from electronic annotation///0016021 // integral component of membrane // in
132.59949	110.72405	NM_029857	///XM_OI	0.005	-1.26		<i>Tmco4</i>	transmembrane and coiled-coil domains 4	0048511 // rhythmic process // inferred from electronic annotation
208.34454	171.5037	NM_027323	///XM_OI	0.006	-1.26		<i>Srrd</i>	SRR1 domain containing	0006470 // protein dephosphorylation // inferred from direct assay
80.88303	67.87937	NM_027982	///XM_OI	0.006	-1.26		<i>Ppm1j</i>	protein phosphatase 1J	0001667 // amoeboid cell migration // not recorded///0007049 // cell cycle // inferred from electronic annotation
267.62848	216.19978	NM_028448	///XM_OI	0.003	-1.27		<i>Cenpv</i>	centromere protein V	0001881 // receptor recycling // not recorded///0007032 // endosome organization // not recorded///0042147 //
118.02771	99.15969	NM_177391	///XM_OI	0.002	-1.27		<i>Fam109b</i>	family with sequence similarity 109, member B	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transci
32.795536	25.93246	NM_0219929	///XA	0.009	-1.27		<i>Zmynd15</i>	zinc finger, MYND-type containing 15	0001816 // cytokine production // inferred from direct assay///0002376 // immune system process // inferred fro
103.3836	86.55347	NM_029926	///NM	0.006	-1.27		<i>Irak4</i>	interleukin-1 receptor-associated kinase 4	0016180 // snRNA processing // not recorded
404.31158	319.5324	NM_001253731	///NM	0.004	-1.27		<i>Ints9</i>	integrator complex subunit 9	0006450 // regulation of translational fidelity // inferred from electronic annotation
511.71274	402.5081	NM_001163454	///NM	0.008	-1.27		<i>Prorsd1</i>	prolyl-tRNA synthetase domain containing 1	0005488 // binding // inferred from electronic annotation///0044822 // poly(A) RNA binding // not recorded
148.44363	123.3462	NM_145432	///XM_OI	0.007	-1.27		<i>Heatr6</i>	HEAT repeat containing 6///Mus musculus HEAT repeat containing 6 (Heatr6), mRN	0007165 // signal transduction // inferred from electronic annotation///0007186 // G-protein coupled receptor sig
60.447395	49.469555	NM_009314	///NM	0.003	-1.27		<i>Tacr2</i>	tachykinin receptor 2	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transci
108.19862	90.95807	NM_030060	///XM_OI	0.005	-1.27		<i>Batf3</i>	basic leucine zipper transcription factor, ATF-like 3	0005525 // GTP binding // inferred from electronic annotation
294.87262	235.92267	NM_174960	///NM	0.004	-1.27		<i>Gimap9</i>	GTPase, IMAP family member 9	0006364 // rRNA processing // inferred from electronic annotation///0042254 // ribosome biogenesis // inferred f
1913.2892	1485.0658	NM_028632	///NM	0.007	-1.27		<i>Fcf1</i>	FCF1 small subunit (SSU) processome component homolog (S. cerevisiae)	0006886 // intracellular protein transport // inferred from electronic annotation///0007340 // acrosome reaction //
607.50995	472.9059	NM_001286033	///NM	0.006	-1.27		<i>Stx2</i>	syntaxin 2	0006139 // nucleobase-containing compound metabolic process // inferred from electronic annotation///0032259
67.4342	55.28693	NM_176917	///XM_OI	0.007	-1.27		<i>Mettl4</i>	methyltransferase like 4	0006915 // apoptotic process // inferred from electronic annotation///0007049 // cell cycle // inferred from electr
1108.5682	865.7077	NM_026455	///NM	0.006	-1.27		<i>Fam32a</i>	family with sequence similarity 32, member A	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transci
81.807014	67.638535	NM_020596	///NM	0.006	-1.28		<i>Egr4</i>	early growth response 4	0007015 // actin filament organization // inferred from direct assay///0007507 // heart development // inferred fr
1756.3993	1353.6064	NM_016798	///XM_OI	0.006	-1.28		<i>Pdlim3</i>	PDZ and LIM domain 3	0006119 // oxidative phosphorylation // not recorded///0006754 // ATP biosynthetic process // not recorded///OC
945.5018	730.1995	NM_001217174	///NM	0.003	-1.28		<i>Surf1</i>	surfeit gene 1	0005515 // protein binding // inferred from electronic annotation///0042802 // identical protein binding // inferre
238.46631	192.21892	NM_029321	///XM_OI	0.002	-1.28		<i>Ttc32</i>	tetratricopeptide repeat domain 32	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transci
474.50665	371.48984	NM_152895	///XM_OI	0.006	-1.28		<i>Kdm5b</i>	lysine (K)-specific demethylase 5B	0007018 // microtubule-based movement // traceable author statement///0008088 // axon cargo transport // infe
140.98708	117.24186	NM_008451	///NR_O4	0.008	-1.28		<i>Klc2</i>	kinesin light chain 2	0030030 // cell projection organization // inferred from electronic annotation///0042384 // cilium assembly // not
362.21988	284.94547	NM_025455	///XM_OI	0.004	-1.28		<i>Cdc28b</i>	coiled coil domain containing 28B	0005515 // protein binding // inferred from electronic annotation
52.466618	41.99371	NM_001081971	///NM	0.005	-1.28		<i>Ankrd63</i>	ankyrin repeat domain 63	0007275 // multicellular organismal development // inferred from electronic annotation
482.1801	375.5232	NM_021436	///XM_OI	0.005	-1.28		<i>Tmeff1</i>	transmembrane protein with EGF-like and two follistatin-like domains 1	0006200 // ATP catabolic process // not recorded///0006810 // transport // inferred from electronic annotation///
457.9985	357.0014	NM_028493	///XM_OI	0.007	-1.28		<i>Rhobtb3</i>	Rho-related BTB domain containing 3	0006584 // catecholamine metabolic process // inferred from electronic annotation///0042135 // neurotransmitte
909.24036	703.30695	NM_173740	///NM	0.009	-1.28		<i>Maoa</i>	monoamine oxidase A	0007049 // cell cycle // inferred from electronic annotation///0007126 // meiotic nuclear division // inferred from
775.07916	597.96216	NM_001168244	///NM	0.010	-1.28		<i>Syce2</i>	synaptonemal complex central element protein 2	0002523 // leukocyte migration involved in inflammatory response // not recorded///0002675 // positive regulatic
529.28296	412.5257	NM_009675	///XM_OI	0.006	-1.28		<i>Aoc3</i>	amine oxidase, copper containing 3	0035556 // intracellular signal transduction // inferred from electronic annotation
978.7117	752.5945	NM_030131	///NM	0.003	-1.28		<i>Cnih4</i>	cornichon homolog 4 (Drosophila)	0006810 // transport // inferred from electronic annotation///0009725 // response to hormone // inferred from di
52.12504	41.544483	NM_033145	///NM	0.008	-1.28		<i>Lcn8</i>	lipocalin 8	0006620 // posttranslational protein targeting to membrane // traceable author statement///0006810 // transport
101.99454	84.24645	NM_008035	///XM_OI	0.004	-1.28		<i>Folr2</i>	folate receptor 2 (fetal)	0001932 // regulation of protein phosphorylation // inferred from mutant phenotype///0006351 // transcription, t
212.474	171.83119	NM_133932	///XM_OI	0.009	-1.28		<i>Tada3</i>	transcriptional adaptor 3	0000413 // protein peptidyl-prolyl isomerization // inferred from electronic annotation///0006397 // mRNA proces
460.60928	358.6683	NM_001285826	///NM	0.004	-1.28		<i>Ppil3</i>	peptidylprolyl isomerase (cyclophilin)-like 3	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transci
1726.8342	1324.4606	NM_021519	///XM_OI	0.004	-1.28		<i>Edf1</i> /// <i>Gm11964</i>	endothelial differentiation-related factor 1///predicted gene 11964	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transci
1726.8342	1324.4606	NM_021519	///XM_OI	0.004	-1.28		<i>Edf1</i> /// <i>Gm11964</i>	endothelial differentiation-related factor 1///predicted gene 11964	0007264 // small GTPase mediated signal transduction // inferred from electronic annotation///0007265 // Ras pr
1353.7998	1038.3312	NM_001166493	///NM	0.008	-1.28		<i>Rasgrp3</i>	RAS, guanyl releasing protein 3	0000038 // very long-chain fatty acid metabolic process // not recorded///0000038 // very long-chain fatty acid ac
34.8133	27.217539	NM_053178	///XM_OI	0.010	-1.28		<i>Acsbg1</i>	acyl-CoA synthetase bubblegum family member 1	0006412 // translation // inferred from electronic annotation
556.77026	432.66962	NM_078479	///XM_OI	0.004	-1.29		<i>Mrps21</i>	mitochondrial ribosomal protein S21	0042417 // dopamine metabolic process // not recorded///0046928 // regulation of neurotransmitter secretion //
102.587	84.5812	NM_001199151	///NM	0.002	-1.29		<i>Sncalp</i>	synuclein, alpha interacting protein (synphilin)	0032981 // mitochondrial respiratory chain complex I assembly // not recorded///0070584 // mitochondrion morp
633.3487	488.12845	NM_029760	///XM_OI	0.007	-1.29		<i>Nubpl</i>	nucleotide binding protein-like	0005515 // protein binding // inferred from electronic annotation
167.7549	138.43306	NM_001081441	///NM	0.008	-1.29		<i>Wdr86</i>	WD repeat domain 86	0007049 // cell cycle // inferred from electronic annotation///0007059 // chromosome segregation // not recorded
121.73956	100.23331	NM_013848	///XM_OI	0.008	-1.29		<i>Ermap</i>	erythroblast membrane-associated protein	0001662 // behavioral fear response // traceable author statement///0007165 // signal transduction // inferred fr
325.30963	254.96643	NM_028232	///XM_OI	0.007	-1.29		<i>Sgol1</i>	shugoshin-like 1 (S. pombe)	0006260 // DNA replication // not recorded///0016477 // cell migration // not recorded///0016567 // protein ubiq
40.117584	31.673004	NM_001160353	///XR	0.006	-1.29		<i>Grm2</i> /// <i>LOC102636702</i>	glutamate receptor, metabotropic 2///uncharacterized LOC102636702	0006457 // protein folding // inferred from electronic annotation///00050790 // regulation of catalytic activity // inl
117.50854	97.1269	NM_172747	///XM_OI	0.005	-1.29		<i>Kctd13</i>	potassium channel tetramerisation domain containing 13	
1548.231	1186.4258	NM_024478	///NM	0.008	-1.29		<i>Grpel1</i>	GrpE-like 1, mitochondrial	

[Nrf2-KO, Air, PBS]	[Nrf2-KO, Air, SFN]	RefSeq	Transcript ID	p	FC	SFN	Gene Symbol	Gene Title	Gene Ontology
476.4157	369.01642	NM_013586		0.002	-1.29		<i>Loxl3</i>	lysyl oxidase-like 3	0001837 // epithelial to mesenchymal transition // not recorded /// 0006898 // receptor-mediated endocytosis // inferred from electronic annotation
114.405396	94.29895	NM_028825	///XM_0	0.005	-1.29		<i>Tex37</i>	testis expressed 37	0005634 // nucleus // inferred from electronic annotation
125.175735	102.549065	NM_172462		0.004	-1.29		<i>Zfp11</i>	zinc finger protein 11	0006355 // regulation of transcription, DNA-templated // not recorded
195.63348	158.35936	NM_026144		0.003	-1.29		<i>Dhdds</i>	dehydrodolichyl diphosphate synthase	0006488 // protein glycosylation // inferred from electronic annotation /// 0008152 // metabolic process // inferred from electronic annotation
149.88881	122.41641	NM_001293791	///NM	0.001	-1.29		<i>Ints10</i>	integrator complex subunit 10	0016180 // snRNA processing // not recorded
250.27039	198.5933	NM_001110017	///NM	0.002	-1.29		<i>Dzip3</i>	DAZ interacting protein 3, zinc finger	0000209 // protein polyubiquitination // not recorded /// 0016567 // protein ubiquitination // inferred from electronic annotation
90.20711	73.66294	NM_174877	///XM_0	0.003	-1.29		<i>Zar1</i>	zygote arrest 1	0007275 // multicellular organismal development // inferred from electronic annotation
25.734549	19.6784	NM_130457	///XM_0	0.004	-1.29		<i>Cntnap4</i>	contactin associated protein-like 4	0007155 // cell adhesion // inferred from electronic annotation /// 0032225 // regulation of synaptic transmission, i
509.5329	391.52274	NM_001284409	///NM	0.006	-1.29		<i>Casp3</i>	caspase 3	0001782 // B cell homeostasis // inferred from mutant phenotype /// 0001836 // release of cytochrome c from mitc
76.96827	62.538654	NM_009779		0.004	-1.30		<i>C3ar1</i>	complement component 3a receptor 1	0002430 // complement receptor mediated signaling pathway // not recorded /// 0002462 // tolerance induction t
202.84416	163.37778	NM_027122		0.005	-1.30		<i>Mfsd3</i>	major facilitator superfamily domain containing 3	0006810 // transport // inferred from electronic annotation /// 0055085 // transmembrane transport // inferred fr
107.17194	87.640625	NM_009767	///XM_0	0.006	-1.30		<i>Chic1</i>	cysteine-rich hydrophobic domain 1	0005886 // plasma membrane // inferred from electronic annotation /// 0016020 // membrane // inferred from ele
109.01	89.50757	NM_024171	///XM_0	0.009	-1.30		<i>LOC101055909</i> /// <i>Sec61b</i>	protein transport protein Sec61 subunit beta-like /// Sec61 beta subunit	0000060 // protein import into nucleus, translocation // not recorded /// 0006810 // transport // inferred from elec
382.34888	296.6227	NM_013841		0.003	-1.30		<i>Vps45</i>	vacuolar protein sorting 45 (yeast)	0006810 // transport // inferred from electronic annotation /// 0006904 // vesicle docking involved in exocytosis //
867.3517	662.38306	NM_026616		0.002	-1.30		<i>Rnaseh2c</i>	ribonuclease H2, subunit C	0006401 // RNA catabolic process // not recorded
501.81345	385.24234	NM_197987	///XM_0	0.003	-1.30		<i>Trim37</i>	tripartite motif-containing 37	0016567 // protein ubiquitination // inferred from electronic annotation /// 0032088 // negative regulation of NF- κ
183.90825	149.64224	NM_178732	///XM_0	0.009	-1.30		<i>Zfp324</i>	zinc finger protein 324	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
2115.042	1600.8473	NM_007483		0.007	-1.30		<i>Rhob</i>	ras homolog gene family, member B	0000910 // cytokinesis // not recorded /// 0001525 // angiogenesis // inferred from electronic annotation /// 000618
18.135279	13.792897	NM_001282054	///NM	0.009	-1.30		<i>Msh4</i>	mutS homolog 4 (E. coli)	0001541 // ovarian follicle development // inferred from mutant phenotype /// 0006200 // ATP catabolic process //
17.628971	13.596579	NR_045271	///XR_37i	0.004	-1.30		<i>Fcor</i>	Foxo1 corepressor	0001659 // temperature homeostasis // inferred from mutant phenotype /// 0001678 // cellular glucose homeosta
53.980125	42.4273			0.003	-1.30		<i>Cdc42os</i>	coiled-coil domain containing 42, opposite strand	
169.78061	138.70511	NM_020505	///NM_1	0.004	-1.30		<i>Vav3</i>	vav 3 oncogene	0001525 // angiogenesis // inferred from electronic annotation /// 0006906 // vesicle fusion // inferred from geneti
328.12732	254.36638	NM_025784	///XM_0	0.003	-1.30		<i>Bcs1l</i>	BCS1-like (yeast)	0007005 // mitochondrion organization // not recorded /// 0008152 // metabolic process // inferred from electroni
156.58208	127.365	NM_001008700	///NM	0.006	-1.30		<i>Il4ra</i>	interleukin 4 receptor, alpha	0002376 // immune system process // inferred from electronic annotation /// 0002532 // production of molecular r
221.88066	176.4187	NM_028713	///XM_0	0.009	-1.30		<i>Rftn2</i>	ratfin family member 2	0033227 // dsRNA transport // inferred from mutant phenotype /// 0043330 // response to exogenous dsRNA // inf
185.7343	150.49617	NM_001163495	///NM	0.006	-1.30		<i>Arhgap19</i>	Rho GTPase activating protein 19	0007165 // signal transduction // inferred from electronic annotation /// 0043547 // positive regulation of GTPase a
171.35478	138.85974	NM_019726	///XM_0	0.003	-1.30		<i>Gps2</i>	G protein pathway suppressor 2	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded /// 0046329 // ne
126.33621	103.3327	NM_013415		0.007	-1.30		<i>Atp1b2</i>	ATPase, Na ⁺ /K ⁺ transporting, beta 2 polypeptide	0006200 // ATP catabolic process // not recorded /// 0006810 // transport // inferred from electronic annotation ///
74.2149	59.768456	NM_001290011	///NM	0.007	-1.30		<i>Pemt</i>	phosphatidylethanolamine N-methyltransferase	0006629 // lipid metabolic process // inferred from electronic annotation /// 0006644 // phospholipid metabolic pr
63.96999	51.13846	NM_183141	///XM_0	0.006	-1.31		<i>Elfn2</i>	leucine rich repeat and fibronectin type III, extracellular 2	0010923 // negative regulation of phosphatase activity // not recorded
102.39672	82.71131	NM_031402	///XM_0	0.009	-1.31		<i>Crispld1</i>	cysteine-rich secretory protein LCCL domain containing 1	0006325 // face morphogenesis // not recorded
44.30608	34.54517			0.009	-1.31		<i>D14Ert016e</i>	DNA segment, Chr 14, ERATO Doi 16, expressed	
2942.6	2202.6	NM_001291108	///NM	0.009	-1.31		<i>Dynlrb1</i>	dynein light chain roadblock-type 1	0006810 // transport // inferred from electronic annotation /// 0007632 // visual behavior // not recorded /// 00081
964.6669	730.3289	NM_001004363		0.007	-1.31		<i>Nuak1</i>	NUAK family, SNF1-like kinase, 1	0006468 // protein phosphorylation // not recorded /// 0006974 // cellular response to DNA damage stimulus // inf
156.2616	125.32957	NM_019833	///XM_0	0.010	-1.31		<i>Fam69b</i>	family with sequence similarity 69, member B	0005783 // endoplasmic reticulum // inferred from electronic annotation /// 0005789 // endoplasmic reticulum me
3318.7725	2497.4377	NM_016753		0.003	-1.31		<i>Lxn</i>	latexin	0006954 // inflammatory response // inferred from electronic annotation /// 0010466 // negative regulation of pep
320.244	247.02145	NM_018797	///XM_0	0.006	-1.31		<i>Plxnc1</i>	plexin C1	0007165 // signal transduction // inferred from electronic annotation /// 0007275 // multicellular organismal devel
384.0148	294.40323	NM_029339		0.002	-1.31		<i>Cdc101</i>	coiled-coil domain containing 101	0006351 // transcription, DNA-templated // inferred from electronic annotation /// 0006355 // regulation of transcr
1307.3048	981.4865	NM_026474		0.002	-1.31		<i>Sugt1</i>	SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae)	0005515 // protein binding // inferred from electronic annotation
358.14755	274.22086	NM_028354	///XM_0	0.002	-1.31		<i>Tdp1</i>	tyrosyl-DNA phosphodiesterase 1	0000012 // single strand break repair // inferred from mutant phenotype /// 0000012 // single strand break repair /
206.38547	163.76834	NM_029037		0.005	-1.31		<i>Pomk</i>	protein-O-mannose kinase	0001764 // neuron migration // inferred from mutant phenotype /// 0006468 // protein phosphorylation // inferre
40.81918	31.549173	NM_001033223	///NM	0.003	-1.32		<i>Lin7a</i>	lin-7 homolog A (C. elegans)	0006810 // transport // inferred from electronic annotation /// 0006887 // exocytosis // inferred from electronic an
321.9184	247.47173	NM_025904		0.004	-1.32		<i>Yae1d1</i>	Yae1 domain containing 1	
1677.59	1258.4897	NM_028260		0.007	-1.32		<i>Immp1</i>	IMP1 inner mitochondrial membrane peptidase-like (S. cerevisiae)	0006508 // proteolysis // inferred from electronic annotation /// 0006627 // protein processing involved in protein
1576.7903	1184.5223	NM_021335		0.002	-1.32		<i>Snrpb2</i>	U2 small nuclear ribonucleoprotein B	0000398 // mRNA splicing, via spliceosome // inferred from electronic annotation /// 0006397 // mRNA processing ,
508.1397	383.1983	NM_026033		0.004	-1.32		<i>Gatad1</i>	GATA zinc finger domain containing 1	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
454.81827	344.5323	NM_025301		0.008	-1.32		<i>Mirpl17</i>	mitochondrial ribosomal protein L17	0000002 // mitochondrial genome maintenance // traceable author statement /// 0006412 // translation // not rec
138.9319	111.432	NM_008961	///XM_0	0.004	-1.32		<i>Pter</i>	phosphotriesterase related	0009056 // catabolic process // inferred from electronic annotation
257.0675	200.38725	NM_001286030	///NM	0.002	-1.32		<i>Dhx32</i>	DEAH (Asp-Glu-Ala-His) box polypeptide 32	0008152 // metabolic process // inferred from electronic annotation
179.49509	143.51959	NM_009062	///XM_0	0.005	-1.32		<i>Rgs4</i>	regulator of G-protein signaling 4	0007186 // G-protein coupled receptor signaling pathway // traceable author statement /// 0009968 // negative reg
470.15674	355.09567	NM_175535	///XM_0	0.002	-1.32		<i>Arhgap20</i>	Rho GTPase activating protein 20	0007165 // signal transduction // inferred from electronic annotation /// 0043547 // positive regulation of GTPase a
34.29709	26.080038	NM_007741		0.002	-1.32		<i>Col9a2</i>	collagen, type IX, alpha 2	0005576 // extracellular region // inferred from electronic annotation /// 0005578 // proteinaceous extracellular m
372.35675	283.19815	NM_028812	///XM_0	0.001	-1.32		<i>Gtf2e1</i>	general transcription factor II E, polypeptide 1 (alpha subunit)	0006351 // transcription, DNA-templated // inferred from electronic annotation /// 0006355 // regulation of transcr
287.86557	222.41658	NM_001004361	///NM	0.002	-1.32		<i>Tpgs2</i>	tubulin polyglutamylation complex subunit 2	0005737 // cytoplasm // inferred from electronic annotation /// 0005856 // cytoskeleton // inferred from electronic
1024.6508	769.35126	NM_001083316	///NM	0.008	-1.32		<i>Pdgfra</i>	platelet derived growth factor receptor, alpha polypeptide	0001553 // luteinization // inferred from genetic interaction /// 0001553 // luteinization // inferred from mutant ph
443.96613	335.73587	NM_025582		0.006	-1.32		<i>Fam213b</i>	family with sequence similarity 213, member B	0001516 // prostaglandin biosynthetic process // inferred from direct assay /// 0006629 // lipid metabolic process /
292.38272	225.41544	NM_027256	///XM_0	0.002	-1.32		<i>Ints4</i>	integrator complex subunit 4	0005488 // binding // inferred from electronic annotation /// 0005515 // protein binding // inferred from electronic
907.28186	679.8016	NM_001164155	///NM	0.006	-1.32		<i>Tnfrsf19</i>	tumor necrosis factor receptor superfamily, member 19	0001942 // hair follicle development // inferred from genetic interaction /// 0043123 // positive regulation of I- κ B
61.947998	48.295303	NR_045780		0.003	-1.33		<i>Zfp652os</i>	zinc finger protein 652, opposite strand	
258.80014	199.8342	NM_001038230	///NM	0.002	-1.33		<i>Anapc11</i>	anaphase promoting complex subunit 11	0007049 // cell cycle // inferred from electronic annotation /// 0007067 // mitotic nuclear division // inferred from
107.020515	85.44347	NM_001035354	///NM	0.006	-1.33		<i>Layn</i>	laylin	0005540 // hyaluronic acid binding // not recorded /// 0030246 // carbohydrate binding // inferred from electronic
1219.4607	908.34406	NM_175526	///XM_0	0.006	-1.33		<i>Clec1a</i>	C-type lectin domain family 1, member a	0030246 // carbohydrate binding // inferred from electronic annotation
91.95072	73.07658	NM_026740		0.002	-1.33		<i>Slc46a1</i>	solute carrier family 46, member 1	0006810 // transport // inferred from electronic annotation /// 0015884 // folic acid transport // not recorded /// 00
205.46031	161.19536	NM_022419		0.010	-1.33		<i>Abhd8</i>	abhydrolase domain containing 8	0008152 // metabolic process // inferred from electronic annotation
582.2013	435.2796	NM_029353	///XM_0	0.006	-1.33		<i>Malsu1</i>	mitochondrial assembly of ribosomal large subunit 1	0042273 // ribosomal large subunit biogenesis // not recorded /// 0070130 // negative regulation of mitochondrial
842.72205	627.8816	NM_146236	///XM_0	0.007	-1.33		<i>Tceal1</i>	transcription elongation factor A (SII)-like 1	0006351 // transcription, DNA-templated // inferred from electronic annotation /// 0006355 // regulation of transcr
184.22528	145.36548	NM_177292		0.002	-1.33		<i>Wscd2</i>	WSC domain containing 2	0016020 // membrane // inferred from electronic annotation /// 0016021 // integral component of membrane // in
332.28314	251.74788	NM_178407	///XM_0	0.009	-1.33		<i>Arap2</i>	ARFgap with RhoGAP domain, ankyrin repeat and PH domain 2	0007165 // signal transduction // inferred from electronic annotation /// 0032312 // regulation of ARF GTPase activ
62.405388	48.419334	NM_013788		0.009	-1.33		<i>Peg12</i>	paternally expressed 12	0005578 // embryonic axis specification // inferred from direct assay /// 0016055 // Wnt signaling pathway // infer
337.7341	256.47308	NM_026933		0.010	-1.33		<i>Triap1</i>	TP53 regulated inhibitor of apoptosis 1	0006810 // transport // inferred from electronic annotation /// 0006869 // lipid transport // inferred from electroni
577.74335	431.9178	NM_027181	///XM_0	0.010	-1.33		<i>Gm6851</i> /// <i>Gm7301</i> /// <i>Pin4</i>	predicted pseudogene 6851 /// predicted gene 7301 /// protein (peptidyl-prolyl cis/tr	0000413 // protein peptidyl-prolyl isomerization // inferred from electronic annotation /// 0006364 // rRNA proces

[Nrf2-KO, Air, PBS] [Nrf2-KO, Air, SFN] RefSeq Transcript ID	p	FC	PBS:SFN	Gene Symbol	Gene Title	Gene Ontology
1507.0249	1115.6831 NM_026027	0.002	-1.33	<i>Pfdn1</i>	prefoldin 1	0006457 // protein folding // inferred from electronic annotation//00021537 // telencephalon development // infe
333.24176	252.68587 NM_198622	0.007	-1.33	<i>H1fx</i>	H1 histone family, member X	0006334 // nucleosome assembly // inferred from electronic annotation
308.87	234.86922 NM_178683//XXM_O	0.006	-1.33	<i>Depdc1b</i>	DEP domain containing 1B	0007165 // signal transduction // inferred from electronic annotation//0035556 // intracellular signal transduction
145.13907	115.28207 NM_019496	0.005	-1.33	<i>Ammecr1</i>	Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region gene 1	0006181 // transport // inferred from electronic annotation//0008152 // metabolic process // inferred from elect
905.43353	674.23114 NM_001038592//NN	0.001	-1.33	<i>Glxr2</i>	glutaredoxin 2 (thioltransferase)	0006281 // DNA repair // inferred from electronic annotation//0006310 // DNA recombination // inferred from el
123.114204	98.10153 NM_177752//XXM_O	0.001	-1.34	<i>Eme1</i>	essential meiotic endonuclease 1 homolog 1 (S. pombe)	0007054 // mitochondrion morphogenesis // inferred from mutant phenotype
631.705	470.5964 NM_026389//XR_38	0.001	-1.34	<i>Poldip2</i>	polymerase (DNA-directed), delta interacting protein 2	0001188 // inactivation of MAPK activity // inferred from direct assay//0006469 // negative regulation of protein
385.67322	290.74564 NM_024438	0.001	-1.34	<i>Dusp19</i>	dual specificity phosphatase 19	0030324 // lung development // inferred from electronic annotation
2123.547	1552.8875 NM_175503	0.007	-1.34	<i>Aard</i>	alanine and arginine rich domain containing protein	0003779 // actin binding // not recorded//0005515 // protein binding // inferred from physical interaction//00051
280.47403	214.833 NM_080451//XXM_O	0.008	-1.34	<i>Synpo2</i>	synaptopodin 2	0003009 // skeletal muscle contraction // not recorded//0006941 // striated muscle contraction // inferred from :
125.17739	99.526985 NM_028001//XXM_O	0.001	-1.34	<i>Jsrp1</i>	junctional sarcoplasmic reticulum protein 1	
444.32578	333.25278 NM_001093759//NN	0.002	-1.34	<i>Trappc13</i>	trafficking protein particle complex 13	
80.734375	63.63642 NM_031183//XXM_O	0.004	-1.34	<i>Gm11532//Sp6</i>	----//Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcr
1090.2358	799.1294 NM_026904//XXM_O	0.001	-1.34	<i>Anapc10</i>	anaphase promoting complex subunit 10	0007049 // cell cycle // inferred from electronic annotation//0007067 // mitotic nuclear division // inferred from
2230.1128	1612.0186 NM_021896//XXM_O	0.003	-1.34	<i>Gucy1a3</i>	guanylate cyclase 1, soluble, alpha 3	0006182 // cGMP biosynthetic process // inferred from mutant phenotype//0006182 // cGMP biosynthetic proce
77.53497	60.74349 NM_001159289//NN	0.007	-1.35	<i>Bcl11a</i>	B cell CLL/lymphoma 11A (zinc finger protein)	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcr
374.49072	280.0011 NM_139291//XXM_O	0.002	-1.35	<i>Cdc26</i>	cell division cycle 26	0007049 // cell cycle // inferred from electronic annotation//0007067 // mitotic nuclear division // inferred from
525.8893	388.74933 NM_146188//XXM_O	0.002	-1.35	<i>Kctd15</i>	potassium channel tetramerisation domain containing 15	0007275 // multicellular organismal development // inferred from electronic annotation//0051260 // protein hom
52.727173	39.983593 NM_144809//XXM_O	0.009	-1.35	<i>Prdm9</i>	PR domain containing 9	0006311 // meiotic gene conversion // not recorded//0006351 // transcription, DNA-templated // inferred from e
155.33177	121.84986 NM_008836//XR_03	0.007	-1.35	<i>Phxr5</i>	per-hexamer repeat gene 5	
22.407635	16.37769 NM_025732//XXM_O	0.001	-1.36	<i>Ankrd61</i>	ankyrin repeat domain 61	0003677 // DNA binding // inferred from electronic annotation//0005515 // protein binding // inferred from elect
34.08868	25.10627 NM_001163691//NN	0.001	-1.36	<i>Cacna1h</i>	calcium channel, voltage-dependent, T type, alpha 1H subunit	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic
121.592545	94.95176 NM_146041//XXM_O	0.002	-1.36	<i>Gmids</i>	GDP-mannose 4, 6-dehydratase	0007219 // Notch signaling pathway // inferred from sequence or structural similarity//0019673 // GDP-mannose
1800.4291	1306.4193 NM_023223	0.006	-1.36	<i>Cdc20</i>	cell division cycle 20	0007049 // cell cycle // inferred from electronic annotation//0007067 // mitotic nuclear division // inferred from
110.34057	85.95164 NM_001122822//NN	0.002	-1.36	<i>Wrn</i>	Werner syndrome homolog (human)	0000723 // telomere maintenance // inferred from genetic interaction//0000723 // telomere maintenance // infe
475.57684	349.3024 NM_001033132//NN	0.009	-1.36	<i>Comm46</i>	COMM domain containing 6	0032088 // negative regulation of NF-kappaB transcription factor activity // not recorded
768.7931	558.8233 NM_025569//NN_O	0.006	-1.36	<i>Mgst3</i>	microsomal glutathione S-transferase 3	0008152 // metabolic process // --//0008152 // metabolic process // inferred from electronic annotation//00055
1736.8685	1260.1621 NM_025387//XXM_O	0.005	-1.36	<i>Tmem14c</i>	transmembrane protein 14C	0006783 // heme biosynthetic process // inferred from electronic annotation
330.44254	246.32713 NM_009791//XXM_O	0.008	-1.36	<i>Aspm</i>	asp (abnormal spindle)-like, microcephaly associated (Drosophila)	0001764 // neuron migration // inferred from genetic interaction//0001764 // neuron migration // inferred from
426.0496	315.11758 NM_001111025//NN	0.001	-1.36	<i>Pigx</i>	phosphatidylinositol glycan anchor biosynthesis, class X	0006506 // GPI anchor biosynthetic process // inferred from electronic annotation
245.00476	184.7495 NM_010255//XXM_O	0.005	-1.36	<i>Gamt</i>	guanineacacetate methyltransferase	0006601 // creatine biosynthetic process // inferred from mutant phenotype//0006601 // creatine biosynthetic p
50.294907	37.466606 NM_008023	0.001	-1.37	<i>Foxb2</i>	forkhead box B2	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0006351 // tri
166.62358	129.84332 NM_008001//XXM_O	0.008	-1.37	<i>Fgd1</i>	FYVE, RhoGEF and PH domain containing 1	0007010 // cytoskeleton organization // inferred from direct assay//0008360 // regulation of cell shape // inferre
439.23337	322.7223 NM_053159	0.006	-1.37	<i>Mrpl3</i>	mitochondrial ribosomal protein L3	0006412 // translation // not recorded
386.2567	284.17725 NM_001190448//NN	0.007	-1.37	<i>Ddc</i>	dopa decarboxylase	0006520 // cellular amino acid metabolic process // inferred from electronic annotation//0007623 // circadian rh
1970.7715	1402.2107 NM_026065//XXM_O	0.003	-1.37	<i>Mrpl42</i>	mitochondrial ribosomal protein L42	0044822 // poly(A) RNA binding // not recorded
225.99126	170.91162 NM_011851	0.009	-1.37	<i>Nt5e</i>	5' nucleotidase, ecto	0006164 // purine nucleotide biosynthetic process // not recorded//0006196 // AMP catabolic process // inferred
537.7537	390.30692 NM_001195338//NN	0.002	-1.37	<i>Bbip1</i>	B5Some interacting protein 1	0042384 // cilium assembly // not recorded//0042755 // eating behavior // inferred from mutant phenotype//00
111.102486	85.97542 NM_178793//XXM_O	0.002	-1.37	<i>Ccbe1</i>	collagen and calcium binding EGF domains 1	0001525 // angiogenesis // inferred from electronic annotation//0001946 // lymphangiogenesis // inferred from
569.5305	412.53387 NM_011917//XXM_O	0.001	-1.37	<i>Xrn2</i>	5'-3' exoribonuclease 2	0000738 // DNA catabolic process, exonucleolytic // not recorded//0006139 // nucleobase-containing compound
327.6235	241.07658 NM_028133	0.002	-1.38	<i>Egln3</i>	egl-9 family hypoxia-inducible factor 3	0001666 // response to hypoxia // not recorded//0006915 // apoptotic process // inferred from electronic annota
161.39618	124.33198 NM_001164573//NN	0.008	-1.38	<i>Myo1h</i>	myosin 1H	0008152 // metabolic process // inferred from electronic annotation
127.47597	98.30433 NM_011845//XXM_O	0.004	-1.38	<i>Mid2</i>	midline 2	0016567 // protein ubiquitination // inferred from electronic annotation//0032897 // negative regulation of viral
96.04039	73.03002 NM_029942	0.010	-1.38	<i>Prelid2</i>	PRELI domain containing 2	0015914 // phospholipid transport // not recorded
103.34752	78.79734 NM_001081407//NN	0.007	-1.38	<i>Plb1</i>	phospholipase B1	0006629 // lipid metabolic process // inferred from electronic annotation//0006644 // phospholipid metabolic pr
416.43024	302.74265 NM_175432	0.000	-1.39	<i>Tmem132c</i>	transmembrane protein 132C	0010923 // negative regulation of phosphatase activity // inferred from sequence or structural similarity
264.32852	196.49113 NM_008137//XXM_O	0.002	-1.39	<i>Gna14</i>	guanine nucleotide binding protein, alpha 14	0006184 // GTP catabolic process // not recorded//0007165 // signal transduction // inferred from electronic ann
331.20117	241.22412 NM_025449	0.001	-1.39	<i>Nicn1</i>	nicotin 1	0005634 // nucleus // inferred from electronic annotation//0005874 // microtubule // inferred from electronic ann
99.15262	75.449936 NM_027010	0.001	-1.39	<i>Crygf</i>	crystallin, gamma F	0001654 // eye development // inferred from mutant phenotype
777.90686	554.2607 NM_020026//XXM_O	0.002	-1.39	<i>B3galnt1</i>	UDP-GalNAc:beta-GlcNAc beta 1,3-galactosaminyltransferase, polypeptide 1	0006486 // protein glycosylation // inferred from electronic annotation//0009312 // oligosaccharide biosynthetic
269.31265	199.10187 NM_016662//XR_38	0.004	-1.39	<i>Mxd3</i>	Max dimerization protein 3	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcr
145.31427	110.45515 NM_001145949//NN	0.005	-1.39	<i>Dlgap5</i>	discs, large (Drosophila) homolog-associated protein 5	0000087 // mitotic M phase // not recorded//0007049 // cell cycle // inferred from electronic annotation//00007
415.23203	301.2986 NM_025566	0.004	-1.39	<i>Tnfrsf811</i>	tumor necrosis factor, alpha-induced protein 8-like 1	
68.68397	51.35937 NM_001142792//NN	0.003	-1.39	<i>Tmem150b</i>	transmembrane protein 150B	0016020 // membrane // inferred from electronic annotation//0016021 // integral component of membrane // in
32.962685	23.446203 NM_007500	0.005	-1.39	<i>Atoh1</i>	atonal homolog 1 (Drosophila)	0001764 // neuron migration // inferred from mutant phenotype//0006351 // transcription, DNA-templated // in
1513.469	1063.2493 NM_001163522//NN	0.006	-1.40	<i>Emcn</i>	endomucin	0001525 // angiogenesis // inferred from sequence or structural similarity//0016337 // single organismal cell-cell
155.33069	117.66943 NM_001013778//XX	0.003	-1.40	<i>Tvp23a</i>	trans-golgi network vesicle protein 23A	0016021 // integral component of membrane // inferred from electronic annotation
2260.7068	1571.7618 NM_027395	0.002	-1.40	<i>Basp1</i>	brain abundant, membrane attached signal protein 1	0045892 // negative regulation of transcription, DNA-templated // not recorded//0045892 // negative regulation
415.6346	299.18332 NM_001135172//NN	0.008	-1.40	<i>C1qtnf7</i>	C1q and tumor necrosis factor related protein 7	0051260 // protein homooligomerization // inferred from direct assay
689.79517	487.75818 NM_175429//XXM_O	0.003	-1.40	<i>Kctd12b</i>	potassium channel tetramerisation domain containing 12b	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic
214.93875	160.29922 NM_029798	0.010	-1.40	<i>Flywch2</i>	FLYWCH family member 2	0044822 // poly(A) RNA binding // not recorded
594.3807	420.10086 NM_009848//XXM_O	0.005	-1.40	<i>Entpd1</i>	ectonucleoside triphosphate diphosphohydrolase 1	0006200 // ATP catabolic process // inferred from direct assay//0007186 // G-protein coupled receptor signaling
216.45532	161.25957 NM_001110162//NN	0.001	-1.40	<i>Cdca2</i>	cell division cycle associated 2	0007049 // cell cycle // inferred from electronic annotation//0007059 // chromosome segregation // inferred from
391.05972	281.36353 NM_172911	0.005	-1.40	<i>D8Erd82e</i>	DNA segment, Chr 8, ERATO Doi 82, expressed	0006468 // protein phosphorylation // inferred from electronic annotation//0016310 // phosphorylation // infern
514.2754	366.67722 NM_031863//XXM_O	0.007	-1.40	<i>Cenpq</i>	centromere protein Q	0000775 // chromosome, centromeric region // inferred from electronic annotation//0005634 // nucleus // not re
123.98846	93.721504 NM_008550//XXM_O	0.007	-1.40	<i>Man2b2</i>	mannosidase 2, alpha B2	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006013 // mannose metabo
154.26088	116.62781 NM_019517//XXM_O	0.001	-1.40	<i>Bace2</i>	beta-site APP-cleaving enzyme 2	0006508 // proteolysis // inferred from electronic annotation//0006509 // membrane protein ectodomain proteo
153.0885	115.90007 NM_029102//XXM_O	0.003	-1.41	<i>Glt8d2</i>	glycosyltransferase 8 domain containing 2	0008152 // metabolic process // inferred from electronic annotation
390.39645	280.12698 NM_001290660//NN	0.008	-1.41	<i>Cd302</i>	CD302 antigen	0006909 // phagocytosis // not recorded
953.11487	669.10876 NM_001285833//NN	0.006	-1.41	<i>Nax4</i>	NADPH oxidase 4	0000902 // cell morphogenesis // inferred from mutant phenotype//0001666 // response to hypoxia // inferred fr
168.86012	126.63981 NM_025864	0.003	-1.41	<i>Tmem206</i>	transmembrane protein 206	0016020 // membrane // inferred from electronic annotation//0016021 // integral component of membrane // in

[Nrf2-KO, Air, PBS]	[Nrf2-KO, Air, SFN]	RefSeq	Transcript ID	p	FC	PBS:SFN	Gene Symbol	Gene Title	Gene Ontology
1962.9341	1367.4845	NM_001012335///NM		0.003	-1.41		Mdk	midkine	0001662 // behavioral fear response // inferred from mutant phenotype///0007275 // multicellular organismal de
470.00073	332.3818	NM_024273///XM_0		0.001	-1.42		Timmcd1	translocase of inner mitochondrial membrane domain containing 1	0005634 // nucleus // not recorded///0005739 // mitochondrion // inferred from direct assay///0005739 // mitoch
385.82672	275.2029	NM_030206		0.007	-1.42		Cygb	cytoglobin	0006810 // transport // inferred from electronic annotation///0006979 // response to oxidative stress // not recor
20.431938	14.452564	NM_178797///XM_0		0.009	-1.42		Far2	fatty acyl CoA reductase 2	0006629 // lipid metabolic process // inferred from electronic annotation///0006694 // steroid biosynthetic proce
238.75812	174.8036	NM_029532///XM_0		0.002	-1.42		Snrnp35	small nuclear ribonucleoprotein 35 (U11/U12)	0006397 // mRNA processing // inferred from electronic annotation///0008380 // RNA splicing // inferred from ele
572.60443	402.72873	NM_026282///XR_37		0.006	-1.42		Spc24	SPC24, NDC80 kinetochore complex component, homolog (S. cerevisiae)	0007049 // cell cycle // inferred from electronic annotation///0007067 // mitotic nuclear division // inferred from
75.08952	55.27078	NM_029741///XM_0		0.001	-1.42		Ppflia3	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting prot	0007269 // neurotransmitter secretion // not recorded///0048172 // regulation of short-term neuronal synaptic pl
66.133415	47.96016	NM_001040695///NM		0.003	-1.42		Uevld	UEV and lactate/malate dehydrogenase domains	0005975 // carbohydrate metabolic process // inferred from electronic annotation///0006464 // cellular protein m
171.16832	127.0191	NM_001081328		0.001	-1.42		Chsy3	chondroitin sulfate synthase 3	0008152 // metabolic process // inferred from electronic annotation
333.6103	236.88177	NM_001161618///NM		0.000	-1.42		Cul5	culin 5	0006511 // ubiquitin-dependent protein catabolic process // inferred from electronic annotation///0006970 // res
738.95154	513.9807	NM_173047		0.001	-1.42		Cbr3	carbonyl reductase 3	0008152 // metabolic process // inferred from electronic annotation///0042376 // phyloquinone catabolic proces
220.60121	161.55362	NM_025962		0.010	-1.43		Mmachc	methylmalonic aciduria cblC type, with homocystinuria	0009236 // cobalamin biosynthetic process // inferred from electronic annotation
151.97545	112.48833	NM_152817///XM_0		0.001	-1.43		Ttc27	tetratricopeptide repeat domain 27	0005515 // protein binding // inferred from electronic annotation
301.6617	216.92056	NM_001290430///NM		0.005	-1.43		Ftsj1	FtsJ homolog 1 (E. coli)	0001510 // RNA methylation // inferred from electronic annotation///0002128 // tRNA nucleoside ribose methylat
147.6291	108.6102	NM_026992///NR_03		0.008	-1.43		Onajc24	Dnaj (Hsp40) homolog, subfamily C, member 24	0006810 // transport // inferred from electronic annotation///0017183 // peptidyl-dipthamide biosynthetic proce
1268.8545	873.6018	NM_007428		0.002	-1.43		Agt	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	0001543 // ovarian follicle rupture // inferred from mutant phenotype///0001568 // blood vessel development // i
279.01852	199.68459	NM_007467		0.004	-1.43		Apip1	amyloid beta (A4) precursor-like protein 1	0006378 // mRNA polyadenylation // inferred from direct assay///0006417 // regulation of translation // inferred f
360.3249	252.59795	NM_001079847///NM		0.008	-1.43		Gpr64	G protein-coupled receptor 64	0007165 // signal transduction // inferred from electronic annotation///0007166 // cell surface receptor signaling i
107.3546	79.08241	NM_007426		0.001	-1.44		Angpt2	angiopoietin 2	0001525 // angiogenesis // inferred from genetic interaction///0001666 // response to hypoxia // inferred from el
113.00433	83.67344	NM_177878		0.002	-1.44		Mblac1	metallo-beta-lactamase domain containing 1	0008152 // metabolic process // inferred from electronic annotation
5645.628	3857.808	NM_053247		0.009	-1.44		Lyve1	lymphatic vessel endothelial hyaluronan receptor 1	0006027 // glycosaminoglycan catabolic process // inferred from direct assay///0006810 // transport // inferred fr
121.45598	89.89753	NM_001012324		0.001	-1.44		Ecm2	extracellular matrix protein 2, female organ and adipocyte specific	0010811 // positive regulation of cell-substrate adhesion // inferred from direct assay///0030198 // extracellular m
891.39557	612.89484	NM_053267		0.004	-1.44		Selm	selenoprotein M	0010269 // response to selenium ion // inferred from mutant phenotype///0035264 // multicellular organism grov
555.9156	384.99414	NM_026526///XM_0		0.001	-1.44		N6amt2	N-6 adenine-specific DNA methyltransferase 2 (putative)	0032259 // methylation // inferred from electronic annotation
250.12187	179.43602	NM_001077713		0.007	-1.44		Acn9	ACN9 homolog (S. cerevisiae)	0005739 // mitochondrion // inferred from electronic annotation///0005758 // mitochondrial intermembrane spa
237.71887	171.39177	NM_178149///XM_0		0.002	-1.44		Pik3ip1	phosphoinositide-3-kinase interacting protein 1	0014067 // negative regulation of phosphatidylinositol 3-kinase signaling // inferred from direct assay///0014067 //
63.661663	45.763233	NM_008764		0.005	-1.44		Tnfrsf11b	tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin)	0006915 // apoptotic process // inferred from electronic annotation///0007165 // signal transduction // inferred fr
339.59152	239.31725	NM_001044741///NM		0.002	-1.44		Cacnb3	calcium channel, voltage-dependent, beta 3 subunit	0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from electronic
268.11597	190.65865	NM_007215		0.004	-1.45		Chst7	carbohydrate (N-acetylglucosamine) sulfotransferase 7	0005975 // carbohydrate metabolic process // inferred from electronic annotation///0006044 // N-acetylglucosam
164.04744	120.011406	NM_001168318///NM		0.007	-1.45		Scara5	scavenger receptor class A, member 5 (putative)	0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from electronic
687.8254	473.63486	NM_053134		0.004	-1.45		Pcdhb9	protocadherin beta 9	0007155 // cell adhesion // inferred from electronic annotation///0007156 // homophilic cell adhesion // inferred
1108.9451	758.71906	NM_054042		0.003	-1.45		Cd248	CD248 antigen, endosalin	0008284 // positive regulation of cell proliferation // inferred from mutant phenotype///0016477 // cell migration
137.27562	100.30771	NM_011427		0.007	-1.45		Snai1	snail family zinc finger 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay///0
68.82652	49.30296	NM_001166645		0.001	-1.45		Zfp882	zinc finger protein 882	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
81.829	59.284855	NM_001035509///NM		0.000	-1.45		Zcchc18	zinc finger, CCHC domain containing 18	0030509 // BMP signaling pathway // not recorded
185.50455	135.20992	NM_019438///XR_37		0.007	-1.45		Ncapg	non-SMC condensin I complex, subunit G	0007076 // mitotic chromosome condensation // not recorded
690.9488	471.4112	NM_008005///NR_1C		0.000	-1.45		Fgf18	fibroblast growth factor 18	0001503 // ossification // inferred from mutant phenotype///0001525 // angiogenesis // inferred from mutant phe
265.34882	188.1758	NM_001033409///XM		0.002	-1.46		Lgr6	leucine-rich repeat-containing G protein-coupled receptor 6	0007165 // signal transduction // inferred from electronic annotation///0007186 // G-protein coupled receptor sig
483.5801	331.87967	NM_008289		0.003	-1.46		Hsd11b2	hydroxysteroid 11-beta dehydrogenase 2	0001666 // response to hypoxia // inferred from electronic annotation///0002017 // regulation of blood volume by
23.81685	16.12452	NM_178678		0.009	-1.46		Lrrtm3	leucine rich repeat transmembrane neuronal 3	1902004 // positive regulation of beta-amyloid formation // inferred from mutant phenotype///1902004 // positiv
342.65283	238.53189	NM_009773///XM_0		0.008	-1.46		Bub1b	budding uninhibited by benzimidazoles 1 homolog, beta (S. cerevisiae)	0006468 // protein phosphorylation // inferred from electronic annotation///0006915 // apoptotic process // infer
78.83165	56.429066	NM_001081224///XM		0.004	-1.46		Prr16	proline rich 16	
283.43787	199.3061	NM_024245///XM_0		0.005	-1.46		Klf23	kinasin family member 23	0000910 // cytokinesis // not recorded///0007018 // microtubule-based movement // inferred from electronic anr
63.59395	44.91379	NM_001166631///NM		0.001	-1.47		Havcr1	hepatitis A virus cellular receptor 1	0033005 // positive regulation of mast cell activation // inferred from direct assay
272.941	191.12143	NM_029790///XM_0		0.004	-1.47		Mettl15	methyltransferase like 15	0032259 // methylation // inferred from electronic annotation
109.840904	79.17547	NR_028264		0.000	-1.47		Dleu2	deleted in lymphocytic leukemia, 2	0010977 // negative regulation of neuron projection development // inferred from genetic interaction///0014043,
69.909775	49.55919	NM_010692		0.000	-1.47		Lbx2	ladybird homeobox homolog 2 (Drosophila)	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcr
1923.5459	1284.3878	NM_001013753///XM		0.009	-1.47		Pcdh17	protocadherin 17	0007155 // cell adhesion // inferred from electronic annotation///0007156 // homophilic cell adhesion // inferred
127.83292	92.35753	NM_019950		0.001	-1.48		Chst5	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 5	0005975 // carbohydrate metabolic process // inferred from electronic annotation///0006044 // N-acetylglucosam
125.35397	89.58526	NM_182783		0.003	-1.48		Fam167b	family with sequence similarity 167, member B	
178.85297	128.3001	NM_001199293///NM		0.001	-1.48		Tex14	testis expressed gene 14	0006468 // protein phosphorylation // inferred from electronic annotation///0007049 // cell cycle // inferred from
771.8504	513.0981	NM_008939		0.002	-1.48		Prss12	protease, serine 12 neurotrypsin (motopsin)	0006508 // proteolysis // inferred from direct assay///0006508 // proteolysis // inferred from mutant phenotype//
348.84506	239.82242	NM_021525///XM_0		0.010	-1.49		Rcl1	RNA terminal phosphate cyclase-like 1	0006364 // rRNA processing // not recorded///0006396 // RNA processing // inferred from electronic annotation//
226.09624	158.50426	NM_001143683///NM		0.001	-1.49		Mpped2	metallophosphoesterase domain containing 2	0008152 // metabolic process // inferred from electronic annotation
208.80586	146.52118	NM_001081114///XM		0.001	-1.50		Clip3	CAP-GLY domain containing linker protein 3	0001934 // positive regulation of protein phosphorylation // inferred from direct assay///0010828 // positive regul
248.34535	172.27098	NM_001168475///NM		0.008	-1.50		Ttc23	tetratricopeptide repeat domain 23	0005515 // protein binding // inferred from electronic annotation
101.84433	71.86929	NM_172951///XM_0		0.009	-1.50		Sntg2	syntrophin, gamma 2	0003779 // actin binding // inferred from electronic annotation///0005515 // protein binding // inferred from elec
554.669	366.9357	NM_178753		0.000	-1.50		Spin4	spindlin family, member 4	0007276 // gamete generation // inferred from electronic annotation
94.122795	65.68825	NM_001271757///NM		0.000	-1.51		Wnt5b	wingless-type MMTV integration site family, member 5B	0002062 // chondrocyte differentiation // inferred from electronic annotation///0007165 // signal transduction //
278.63016	191.40471	NM_001289487///NM		0.005	-1.51		Exoc314	exocyst complex component 3-like 4	0006887 // exocytosis // inferred from electronic annotation
265.62103	181.28967	NM_009364///XM_0		0.004	-1.52		Tjp2	tissue factor pathway inhibitor 2	0007596 // blood coagulation // inferred from electronic annotation///0007599 // hemostasis // inferred from ele
1151.1533	758.62775	NM_010423///XM_0		0.009	-1.52		Hcy1	hair/enhancer-of-split related with YRPW motif 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay///0
214.86055	148.62045	NM_001110512///NM		0.001	-1.52		Mettl8	methyltransferase like 8	0007519 // skeletal muscle tissue development // inferred from direct assay///0008152 // metabolic process // inf
463.74387	306.95325	NM_001033331///NM		0.010	-1.52		Gas2l3	growth arrest-specific 2 like 3	0000226 // microtubule cytoskeleton organization // not recorded///0007050 // cell cycle arrest // inferred from
101.85328	70.21146	NM_001127233///NM		0.005	-1.52		Trp53	transformation related protein 53	0000060 // protein import into nucleus, translocation // inferred from direct assay///0000122 // negative regulati
93.869415	64.52021	NM_010460///NM_0		0.008	-1.52		Hoxb7//Hoxb8	homeobox B7//homeobox B8	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcr
42.14293	27.84835	NM_001081651///XM		0.005	-1.53		Rab42	RAB42, member RAS oncogene family	0007264 // small GTPase mediated signal transduction // inferred from electronic annotation///0015031 // protei
3557.841	2307.1895	NM_032398		0.000	-1.53		Pivap	plasmalemma vesicle associated protein	0000165 // MAPK cascade // not recorded///0002693 // positive regulation of cellular extravasation // inferred fr
2217.2612	1414.6968	NM_001008497///NM		0.004	-1.53		P2ry14	purinergic receptor P2Y, G-protein coupled, 14	0006955 // immune response // not recorded///0007165 // signal transduction // inferred from electronic annotat
133.75133	93.684616	NM_013811///XM_0		0.009	-1.53		Onah8	dynein, axonemal, heavy chain 8	0006200 // ATP catabolic process // inferred from electronic annotation///0007018 // microtubule-based moveme
110.893295	76.06643	NM_009116///XM_0		0.005	-1.53		Prrx2	paired related homeobox 2	0002053 // positive regulation of mesenchymal cell proliferation // inferred from genetic interaction///0006355 //

[Nrf2-KO, Air, PBS]	[Nrf2-KO, Air, SFN]	RefSeq Transcript ID	p	FC PBS:SFN	Gene Symbol	Gene Title	Gene Ontology
152.97404	105.081436	NM_011270	0.000	-1.54	<i>Rhd</i>	Rh blood group, D antigen	0015696 // ammonium transport // inferred from mutant phenotype//0048821 // erythrocyte development // inferred from electronic annotation
226.04362	154.1083	NM_013552//XM_01	0.002	-1.54	<i>Hmnmr</i>	hyaluronan mediated motility receptor (RHAMM)	0000160 // phosphorelay signal transduction system // inferred from electronic annotation
208.20135	142.04077	NM_011943//XM_01	0.006	-1.54	<i>Map2k6</i>	mitogen-activated protein kinase kinase 6	0000165 // MAPK cascade // not recorded//0000165 // MAPK cascade // inferred from physical interaction//0000097237 // cellular response to toxic substance // inferred from mutant phenotype
235.67747	158.48277	NM_178890	0.007	-1.55	<i>Abtb2</i>	ankyrin repeat and BTB (POZ) domain containing 2	0005975 // carbohydrate metabolic process // inferred from electronic annotation
66.024605	43.979137	NM_001081257//XM_01	0.005	-1.56	<i>Hpse2</i>	heparanase 2	0006816 // calcium ion transport // inferred from direct assay//0006935 // chemotaxis // inferred from direct assay
96.50908	65.044495	NM_001281859//NM_01	0.002	-1.56	<i>Cysltr1</i>	cysteinyl leukotriene receptor 1	0005576 // extracellular region // inferred from electronic annotation
106.63459	72.27501	NM_001039554//XM_01	0.002	-1.56	<i>Angptl7</i>	angiotensin-like 7	0000209 // protein polyubiquitination // not recorded//0009411 // response to UV // inferred from direct assay//0006810 // transport // inferred from electronic annotation//0006869 // lipid transport // inferred from direct assay
459.28854	296.07187	NM_001161782//NM_01	0.002	-1.57	<i>Trim32</i>	tripartite motif-containing 32	0000132 // establishment of mitotic spindle orientation // inferred from genetic interaction//0000187 // activation of cell cycle // not recorded
2627.7434	1645.6454	NM_026730//XM_01	0.003	-1.57	<i>Gpihbp1</i>	GPI-anchored HDL-binding protein 1	0007059 // chromosome segregation // not recorded
148.71043	100.89615	NM_008002	0.001	-1.57	<i>Fgf10</i>	fibroblast growth factor 10	0001666 // response to hypoxia // inferred from mutant phenotype//0006508 // proteolysis // inferred from direct assay
1063.8348	666.0999	NM_026753	0.007	-1.59	<i>Fam96b</i>	family with sequence similarity 96, member B	0001764 // neuron migration // inferred from genetic interaction//0001764 // neuron migration // inferred from direct assay
554.43036	349.15582	NM_008872//XM_01	0.003	-1.59	<i>Plat</i>	plasminogen activator, tissue	0010906 // regulation of glucose metabolic process // inferred from direct assay//0035774 // positive regulation of cell cycle // not recorded
77.80748	51.41216	NM_010014//NM_01	0.001	-1.59	<i>Dab1</i>	disabled 1	0006730 // one-carbon metabolic process // inferred from electronic annotation//0006979 // response to oxidative stress // not recorded
908.5482	561.06116	NM_026125//XM_01	0.007	-1.60	<i>Fam132a</i>	family with sequence similarity 132, member A	0001649 // osteoblast differentiation // inferred from expression pattern//0001775 // cell activation // not recorded
65.46931	41.820446	NM_007606	0.001	-1.60	<i>Car3</i>	carbonic anhydrase 3	0008152 // metabolic process // inferred from electronic annotation//0010800 // positive regulation of peptidyl-tyrosine phosphorylation // not recorded
2056.5046	1261.5541	NM_001111274//NM_01	0.004	-1.61	<i>Igf1</i>	insulin-like growth factor 1	0000166 // nucleotide binding // inferred from electronic annotation//0003676 // nucleic acid binding // inferred from electronic annotation
102.78103	66.57678	NM_030728//XM_01	0.005	-1.61	<i>Cemip</i>	cell migration inducing protein, hyaluronan binding	0005515 // protein binding // inferred from electronic annotation
331.3779	210.5923	NM_029007	0.001	-1.62	<i>Fam84a</i>	family with sequence similarity 84, member A	0002221 // pattern recognition receptor signaling pathway // not recorded//0002376 // immune system process // inferred from electronic annotation
168.87688	110.31698	NM_001101479//XM_01	0.001	-1.62	<i>Pabpc4l</i>	poly(A) binding protein, cytoplasmic 4-like	0006198 // cAMP catabolic process // not recorded//0007165 // signal transduction // inferred from electronic annotation
65.818535	41.88387	NM_001103367//NM_01	0.000	-1.62	<i>Rai2</i>	retinoic acid induced 2	0002931 // response to ischemia // inferred from mutant phenotype//0006508 // proteolysis // inferred from electronic annotation
128.29865	82.591	NM_001159711//NM_01	0.001	-1.63	<i>Ly96</i>	lymphocyte antigen 96	0000902 // cell morphogenesis // inferred from mutant phenotype//0001816 // cytokine production // inferred from electronic annotation
118.47577	76.61016	NM_001009978//NM_01	0.001	-1.64	<i>Pde1a</i>	phosphodiesterase 1A, calmodulin-dependent	0001570 // vasculogenesis // not recorded//0001666 // response to hypoxia // inferred from electronic annotation
80.8306	51.583954	NM_173425//XM_01	0.002	-1.64	<i>Fam124b</i>	family with sequence similarity 124, member B	0000086 // G2/M transition of mitotic cell cycle // not recorded//0000087 // mitotic M phase // inferred from electronic annotation
94.2049	59.792088	NM_011670	0.007	-1.64	<i>Uchl1</i>	ubiquitin carboxy-terminal hydrolase L1	0071222 // cellular response to lipopolysaccharide // inferred from expression pattern
953.23206	575.52185	NM_001111100//NM_01	0.006	-1.66	<i>Lipa</i>	lysosomal acid lipase A	0006461 // protein complex assembly // not recorded//0008152 // metabolic process // inferred from electronic annotation
340.11542	207.1582	NM_009627	0.004	-1.67	<i>Adm</i>	adrenomedullin	0006915 // apoptotic process // inferred from electronic annotation//0007605 // sensory perception of sound // inferred from electronic annotation
129.80984	81.81148	NM_009860//XM_01	0.005	-1.67	<i>Cdc25c</i>	cell division cycle 25C	0007049 // cell cycle // inferred from electronic annotation//0007067 // mitotic nuclear division // inferred from electronic annotation
95.38972	57.462685	NM_001195084//NM_01	0.005	-1.72	<i>Plscr2</i>	phospholipid scramblase 2	0001889 // liver development // inferred from mutant phenotype//0006351 // transcription, DNA-templated // inferred from electronic annotation
337.92392	200.06259	NM_177157	0.006	-1.74	<i>Gchfr</i>	GTP cyclohydrolase 1 feedback regulator	00119511 // peptidyl-proline hydroxylation // not recorded//0055114 // oxidation-reduction process // not recorded
112.232086	67.218216	NM_018769//XM_01	0.001	-1.75	<i>Dfna5</i>	deafness, autosomal dominant 5 (human)	0006629 // lipid metabolic process // inferred from electronic annotation//0007165 // signal transduction // inferred from electronic annotation
111.56142	66.486885	NM_001042653	0.007	-1.76	<i>Oip5</i>	Opa interacting protein 5	0006091 // generation of precursor metabolites and energy // not recorded//0006200 // ATP catabolic process // inferred from electronic annotation
750.7436	417.03296	NM_008250	0.002	-1.79	<i>Hlx</i>	H2.0-like homeobox	0006470 // protein dephosphorylation // inferred from electronic annotation//0007049 // cell cycle // inferred from electronic annotation
107.776245	63.390053	NM_177161//XM_01	0.009	-1.80	<i>P4ha3</i>	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide	0006829 // zinc ion transport // inferred from direct assay//0030001 // metal ion transport // inferred from electronic annotation
131.0536	76.33556	NM_177355	0.006	-1.84	<i>Plcx3</i>	phosphatidylinositol-specific phospholipase C, X domain containing 3	0008152 // metabolic process // inferred from electronic annotation
254.54904	140.26909	NM_008813//XM_01	0.000	-1.90	<i>Enpp1</i>	ectonucleotide pyrophosphatase/phosphodiesterase 1	0006952 // defense response // non-traceable author statement//0007157 // heterophilic cell-cell adhesion // not recorded
278.44623	152.16171	NM_028222//XM_01	0.001	-1.91	<i>Cdkn3</i>	cyclin-dependent kinase inhibitor 3	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling // not recorded
166.40152	85.868385	NM_001039676//XM_01	0.009	-2.03	<i>Slc39a2</i>	solute carrier family 39 (zinc transporter), member 2	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006054 // N-acetylneuraminic acid metabolic process // not recorded
111.33941	56.383278	NM_173414	0.000	-2.06	<i>Lanc13</i>	LanC lantibiotic synthetase component C-like 3 (bacterial)	0009972 // cytidine deamination // not recorded//0030308 // negative regulation of cell growth // not recorded, inferred from electronic annotation
111.55397	56.51285	NM_023612	0.001	-2.07	<i>Esm1</i>	endothelial cell-specific molecule 1	
2052.631	939.8809	NM_008342//XM_01	0.003	-2.15	<i>Igfbp2</i>	insulin-like growth factor binding protein 2	
140.03244	68.467514	NM_029847//XM_01	0.007	-2.18	<i>Arsk</i>	arylsulfatase K	
224.33	108.98248	NM_173422	0.003	-2.19	<i>Colec10</i>	collectin sub-family member 10	
288.8033	136.99895	NM_144944	0.002	-2.22	<i>Prokr2</i>	prokineticin receptor 2	
53.607018	21.961576	NM_172829//XM_01	0.005	-2.44	<i>St6gal2</i>	beta galactoside alpha 2,6 sialyltransferase 2	
157.1751	66.76568	NM_028176//XM_01	0.001	-2.48	<i>Cda</i>	cytidine deaminase	

Table S3. Prenatal sulforaphane-neonatal hyperoxia interaction 258 genes in *Nrf2*^{-/-} mice (2-Way ANOVA, p<=0.01)

RIKEN cDNA and predicted genes excluded. Fold Change (FC): Blue (-) - fold lower in SFN:O2 than PBS:O2; Red - fold higher in SFN:O2 than PBS:O2.

[ICR, Air, PBS]	[ICR, Air, SFN]	[ICR, O2, PBS]	[ICR, O2, SFN]	RefSeq Transcript ID	p	(Prenatal Treatment-Exposure)	FC [Air-PBS: O2-PBS FC]	[O2 PBS-SFN] Gene Symbol	Gene Title	Gene Ontology	
69.962	72.55377	31.495602	73.17308	NM_0020265//XM_0065			0.005	-2.22	2.32 Dkk2	dickkopf homolog 2 (Xenopus laevis)	0002376 // immune system process // inferred from electronic annotation//0006810 // transpor
1435.3619	1514.5039	329.68805	624.2319	NM_138738//XM_0065			0.002	-4.35	1.89 Prr35	protease, serine 35	0001889 // liver development // inferred from electronic annotation//0006725 // cellular aroma
1782.2644	1798.7755	1049.2744	1986.1266	NM_001198811//NM_1			0.008	-1.70	1.89 Frem1	Fras1 related extracellular matrix protein 1	0007155 // cell adhesion // inferred from electronic annotation//0031016 // pancreas developm
343.08368	283.36444	147.0619	273.31763	NM_019662//XM_0065			0.004	-2.33	1.86 Rad	Ras-related associated with diabetes	0006629 // lipid metabolic process // inferred from electronic annotation//0016042 // lipid catal
12.493289	13.344014	12.067748	21.504776	NM_173427//NR_0355			0.009	-1.04	1.78 Kihdc7a//Mir2139	kelch domain containing 7a//microRNA 2139	0008152 // metabolic process // inferred from electronic annotation//0016310 // phosphorylati
2220.1902	1995.4437	1351.5511	2271.5432	NM_001163577//NM_0			0.007	-1.64	1.68 Prom1	prominin 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from
289.77322	328.9068	393.5178	649.8168	NM_001081322//XM_0			0.002	1.36	1.65 Myo5c	myosin VC	0006468 // protein phosphorylation // not recorded//0006811 // ion transport // inferred from c
14.985249	13.548375	11.287953	18.416538	NR_045273			0.007	-1.33	1.63 Med9s	mediator complex subunit 9, opposite strand	0034220 // ion transmembrane transport // not recorded
182.24828	164.31073	124.71969	200.49524	NM_178908			0.007	-1.46	1.61 Fam26e	family with sequence similarity 26, member E	001656 // metanephros development // inferred from sequence or structural similarity//00016
153.06573	143.52809	98.77891	149.83705	NM_181815//XM_0065			0.008	-1.55	1.52 Cep128	centrosomal protein 128	0009887 // organ morphogenesis // inferred from mutant phenotype//0018149 // peptide cross
285.66928	308.43195	296.21262	443.75516	NM_029022//XM_0065			0.003	1.04	1.50 Scrn3	secernin 3	0007155 // cell adhesion // inferred from electronic annotation//0007156 // homophilic cell adh
38.758457	32.76064	39.00012	57.417824	NM_011136			0.004	1.01	1.47 Pou2af1	POU domain, class 2, associating factor 1	0001503 // ossification // not recorded//0006874 // cellular calcium ion homeostasis // traceabl
414.32886	354.26688	255.0949	375.13043	NM_001146031//NM_1			0.002	-1.62	1.47 Nrcam	neuron-glia-CAM-related cell adhesion molecule	0005576 // extracellular region // inferred from electronic annotation//0005737 // cytoplasm //
212.25095	213.30676	175.44528	257.22845	NM_194269//XM_0065			0.009	-1.21	1.47 Morn2	MORN repeat containing 2	0042552 // myelination // not recorded//1902043 // positive regulation of extrinsic apoptotic sig
21.415405	18.123074	23.46498	34.23301	NM_001013756//XM_0			0.006	1.10	1.46 Grhl3	grainyhead-like 3 (Drosophila)	0044237 // cellular metabolic process // inferred from electronic annotation//0055114 // oxidati
744.06445	696.336	373.4801	542.73157	NM_023245			0.001	-1.99	1.45 Palm	palmdelphin	
274.52957	272.0314	272.9089	388.82977	NM_008884//NM_1780			0.000	-1.01	1.42 Pml	promyelocytic leukemia	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferre
11671.783	11961.448	8171.2534	11585.314	NM_0119759			0.006	-1.43	1.42 Dpt	dermatopontin	0006352 // DNA-templated transcription, initiation // inferred from electronic annotation//0006
2468.152	2428.5479	1506.5468	2106.177	NM_054041//XM_0065			0.008	-1.64	1.40 Antsr1	anthrax toxin receptor 1	0008088 // axon cargo transport // inferred from mutant phenotype//0008152 // metabolic pro
1153.7617	1322.3784	1018.6307	1423.494	NM_007984			0.002	-1.13	1.40 Fcnr1	fascin homolog 1, actin bundling protein (Strongylocentrotus purpuratus)	0008152 // metabolic process // inferred from electronic annotation//0032254 // establishment
235.98412	232.56755	241.1119	329.556	NM_001163464//NM_0			0.009	1.02	1.37 Abi3	ABI gene family, member 3	0006417 // regulation of translation // inferred from electronic annotation//0016070 // RNA mei
313.80157	295.3039	382.37112	522.4244	NM_133234//XM_0065			0.007	1.22	1.37 Bbc3	BCL2 binding component 3	0006355 // regulation of transcription, DNA-templated // not recorded
557.9463	540.34314	537.37665	730.9747	NM_0093151//XM_0065			0.002	-1.04	1.36 Tafj6	TAF6 RNA polymerase II, TATA box binding protein (TBP)-associated factor	0002238 // response to molecule of fungal origin // inferred from mutant phenotype//0002376 /
353.16513	395.15637	369.247	495.5319	NM_017391			0.008	1.05	1.34 Slcsa3	solute carrier family 5 (inositol transporters), member 3	0001934 // positive regulation of protein phosphorylation // not recorded//0002376 // immune
97.9636	104.04598	68.37857	90.27526	NM_031998//XM_0065			0.009	-1.43	1.32 Cep41	centrosomal protein 41	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // reg
276.13083	270.76517	172.2666	226.55972	NM_001081243//XM_0			0.000	-1.60	1.32 Filip1	filamin A interacting protein 1	0006355 // regulation of transcription, DNA-templated // not recorded
158.55287	172.46252	80.823364	106.18038	NM_00110162//NM_1			0.006	-1.96	1.31 Cdc42	cell division cycle associated 2	005739 // mitochondrion // inferred from direct assay//0016020 // membrane // inferred from
147.0618	163.17853	165.08623	216.28656	NM_199449			0.003	1.12	1.31 Zhx2	zinc fingers and homeoboxes 2	0006412 // translation // not recorded
615.59863	645.599	511.9526	669.8806	NM_009288//XM_0065			0.005	-1.20	1.31 Shk1	serine/threonine kinase 10	0006310 // DNA recombination // inferred from electronic annotation//0006810 // transport // i
310.10034	306.23703	250.48381	323.60477	NM_001290701//NM_0			0.008	-1.24	1.29 Meaf6	MYST/Esa1-associated factor 6	0001836 // release of cytochrome c from mitochondria // not recorded//0001836 // release of c
48.34705	41.120743	37.52458	47.858074	NM_144786//XM_0064			0.006	-1.29	1.28 Ggt7	gamma-glutamyltransferase 7	0005515 // protein binding // inferred from physical interaction//0008022 // protein C-terminu
4880.149	4793.979	4049.3477	5153.279	NM_01170981//NM_0			0.000	-1.21	1.27 Hmnpkc	heterogeneous nuclear ribonucleoprotein C	0006928 // cellular component movement // not recorded//0007155 // cell adhesion // not reco
19.93411	17.67726	15.712506	19.89045	NM_025420//XM_0065			0.001	-1.27	1.27 Lec1m	late cornified envelope 1M	0016567 // protein ubiquitination // inferred from electronic annotation
309.1059	247.5186	313.42593	396.6182	NM_153143			0.006	1.01	1.27 Kctd11	potassium channel tetramerisation domain containing 11	0007010 // cytoskeleton organization // inferred from electronic annotation//0051693 // actin fi
1425.3546	1387.6141	1091.5663	1372.098	NM_177715//NR_0395f			0.006	-1.31	1.26 Kctd12//Mir5130	potassium channel tetramerisation domain containing 12//microRNA 5130	0000054 // ribosomal subunit export from nucleus // inferred from electronic annotation//0006
2518.802	2448.97	1718.7509	2158.0605	NM_009450			0.002	-1.47	1.26 Tubb2a	tubulin, beta 2A class IIa	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein cou
730.66693	715.09106	572.08075	943.2594	NM_001130149//NM_0			0.002	1.03	1.25 Droshea	drosha, ribonuclease type III	0000226 // microtubule cytoskeleton organization // not recorded//0010923 // negative regulat
252.06018	245.30936	235.94566	291.79364	NM_026641//XM_0065			0.007	-1.07	1.24 Ift80	intraflagellar transport 80	0006810 // transport // inferred from electronic annotation//0006817 // phosphate ion transpor
240.73627	227.8107	198.6216	243.10745	NM_001165951//NM_1			0.010	-1.21	1.22 Vangl1	vang-like 1 (van gogh, Drosophila)	0016020 // membrane // inferred from electronic annotation//0016021 // integral component o
467.52026	421.4644	506.38968	619.50287	NM_009029//XM_0065			0.010	1.08	1.22 Rb1	retinoblastoma 1	0006412 // translation // inferred from electronic annotation//0032543 // mitochondrial transl
389.43506	343.54913	246.42226	300.32742	NM_177906//XM_0065			0.001	-1.58	1.22 Opclm	opiotin binding protein/cell adhesion molecule-like	0016020 // membrane // inferred from electronic annotation//0016021 // integral component o
1617.7766	1402.6871	563.3106	686.4046	NM_023223			0.004	-2.87	1.22 Cdc20	cell division cycle 20	0006591 // ornithine metabolic process // inferred from direct assay//0006596 // polyamine bio
250.1217	239.53566	204.21277	246.47789	NM_029790//XM_0065			0.006	-1.22	1.21 Mett15	methyltransferase like 15	0016020 // membrane // inferred from electronic annotation//0016021 // integral component o
1382.3983	1401.8483	1098.0057	1320.7719	NM_026057//XM_0065			0.009	-1.26	1.20 Zfp422	zinc finger protein 422	0006464 // cellular protein modification process // inferred from direct assay//0008152 // metal
275.35104	253.32229	253.2326	377.73175	NM_001081054//XR_38			0.003	1.14	1.20 Qrs1	glutaminyl-tRNA synthetase (glutamine-hydrolyzing)-like 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from
234.62373	185.58629	203.69936	343.78697	NM_001162947//NM_0			0.008	-1.15	1.20 Nek3	NIMA (never in mitosis gene a)-related expressed kinase 3	0045454 // cell redox homeostasis // inferred from electronic annotation//0055114 // oxidation-
313.12923	322.58344	324.98703	388.3312	NM_001006122//NM_0			0.007	1.04	1.19 Leo1	Leo1, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferre
1405.0721	1398.3351	1507.5071	1798.3237	NM_010305			0.009	1.07	1.19 Gnao1	guanine nucleotide binding protein (G protein), alpha inhibiting 1	0001916 // positive regulation of T cell mediated cytotoxicity // inferred from direct assay//0001
583.93726	556.37476	2041.3582	2420.064	NM_010145			0.004	3.50	1.19 Ephx1	epoxide hydrolase 1, microsomal	0001736 // establishment of planar polarity // inferred from genetic interaction//0006351 // trar
140.51112	136.01991	142.88734	168.73933	NM_001159948//NM_0			0.009	1.02	1.18 Als2	amyotrophic lateral sclerosis 2 (juvenile)	0015937 // coenzyme A biosynthetic process // inferred from electronic annotation//0016310 //
125.8917	123.12924	110.34735	129.88864	NM_025473//XM_0065			0.009	-1.14	1.18 Fam3a	family with sequence similarity 3, member A	0000082 // G1/S transition of mitotic cell cycle // inferred from mutant phenotype//0000122 // t
92.37111	68.36415	86.19487	101.24989	NM_019577//XM_0065			0.007	-1.07	1.17 Ccl24	chemokine (C-C motif) ligand 24	0006397 // mRNA processing // inferred from electronic annotation//0008380 // RNA splicing //
21.38159	17.56756	13.705908	16.02138	NM_001037906			0.005	-1.56	1.17 Nell1	NEL-like 1	0006184 // GTP catabolic process // not recorded//0007049 // cell cycle // inferred from elect
335.91214	347.8988	289.04532	337.23972	NM_145221//XM_0065			0.001	-1.16	1.17 App1	adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper co	0001824 // blastocyst development // inferred from direct assay
21.299736	19.633522	20.586864	23.849493	NR_003283			0.003	-1.03	1.16 Rab11fp4a51	RAB11 family interacting protein 4 (class II), opposite strand 1	0005737 // cytoplasm // inferred from electronic annotation//0005813 // centrosome // not rec
322.906	281.8248	247.32037	283.85355	NM_001276719//NM_0			0.005	-1.31	1.15 Akr2	atypical chemokine receptor 2	0006184 // GTP catabolic process // not recorded//0006886 // intracellular protein transport // i
265.85815	261.5832	256.9423	294.46765	NM_053177//XR_37867			0.004	-1.03	1.15 Mcoln1	mucopolin 1	0000910 // cytokinesis // not recorded//0006351 // transcription, DNA-templated // inferred fr
44.707375	38.64207	32.335384	36.822876	NM_010050			0.003	-1.38	1.14 Dia2	deiodinase, iodothyronine, type II	0006020 // inositol metabolic process // inferred from mutant phenotype//0006412 // translati
725.8644	656.58636	729.48694	826.66895	NM_001190343//NM_0			0.003	1.00	1.13 Ccm2	cerebral cavernous malformation 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // reg
71.6419	58.942333	57.64307	65.162	NM_026956//XM_0065			0.000	-1.24	1.13 Cd209f	CD209f antigen	0001711 // endodermal cell fate commitment // inferred from mutant phenotype//0006351 // ti
1607.85	1282.958	1874.1724	2114.7388	NM_001177556//NM_0			0.003	1.17	1.13 Gng12	guanine nucleotide binding protein (G protein), gamma 12	0006508 // proteolysis // inferred from electronic annotation
79.64633	65.18264	75.69151	85.17433	NM_013606//NR_0035f			0.009	-1.05	1.13 Mx2	myxovirus (influenza virus) resistance 2	0006370 // 7-methylguanosine mRNA capping // not recorded//0006397 // mRNA processing //
293.9439	267.09634	246.3518	276.8707	NM_001033533			0.005	-1.19	1.12 Cdc4102a	coiled-coil domain containing 102A	0048565 // digestive tract development // not recorded
52.722187	47.619675	40.566326	45.47538	NM_001001985			0.010	-1.30	1.12 Nat8l	N-acetyltransferase 8-like	0001539 // cilium or flagellum-dependent cell motility // inferred from sequence or structural sim
286.68628	266.12122	292.28632	323.16782	NM_028276			0.009	1.02	1.11 Utp14a	UTP14, U3 small nucleolar ribonucleoprotein, homolog A (yeast)	0006396 // RNA processing // inferred from electronic annotation//0010468 // regulation of gen
193.88818	167.13765	164.93602	181.00475	NM_146248			0.008	-1.18	1.10 Cchcr1	coiled-coil alpha-helical rod protein 1	0001525 // angiogenesis // inferred from electronic annotation//0001938 // positive regulation c
278.44363	248.53651	179.86086	195.88142	NM_001004361//NM_0			0.008	-1.55	1.09 Tpgs2	tubulin polyglutamylation complex subunit 2	0018108 // peptidyl-tyrosine phosphorylation // not recorded//0030334 // regulation of cell mig
1635.2136	1568.6636	1344.5557	1459.1736	NM_024189//NR_0283f			0.009	-1.22	1.09 Yaf2	YY1 associated factor 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // reg
93.102594	858.81775	749.127	811.437	NM_009774//XM_0065			0.008	-1.24	1.08 Bub3	budding uninhibited by benzimidazoles 3 homolog (S. cerevisiae)	0006364 // rRNA processing // inferred from electronic annotation//0042254 // ribosome bioger
19.268366	13.963492	15.410205	16.68665	NM_001164682//NM_1			0.006	-1.25	1.08 Mpp4	membrane protein, palmitoylated 4 (MAGUK p55 subfamily member 4)	0001921 // positive regulation of receptor recycling // inferred from direct assay//0006461 // pr
4359.0586	4262.3184	4032.455	4360.5083	NM_133933			0.008	-1.08	1.08 Rpn1	ribophorin I	0007219 // Notch signaling pathway // inferred from electronic annotation//0034976 // respons
262											

[ICR, Air, PBS]	[ICR, Air, SFN]	[ICR, O2, PBS]	[ICR, O2, SFN]	RefSeq Transcript ID	p (Prenatal Treatment-Exposure)	FC [Air-PBS: O2-PBS]	FC [O2 PBS:SFN]	Gene Symbol	Gene Title	Gene Ontology
22.082022	16.430124	18.113605	18.805227	NM_010666		0.006	-1.22	1.04 Krt27	keratin 27	0001568 // blood vessel development // inferred from mutant phenotype//0001570 // vasculog
33.819256	27.008427	29.399582	30.436289	NM_001129803//NM_0		0.005	-1.15	1.04 Pcp2	Purkinje cell protein 2 (L7)	0006355 // regulation of transcription, DNA-templated // not recorded
89.95629	72.791016	77.12211	78.526535	NM_153424//XM_0065		0.004	-1.17	1.02 Nph4p	nephronophthisis 4 (juvenile) homolog (human)	0001666 // response to hypoxia // inferred from mutant phenotype//0001666 // response to hyp
27.035168	21.454285	21.628815	21.964022			0.003	-1.25	1.02 AK007819//Gm13594	Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched libra	0000301 // retrograde transport, vesicle recycling within Golgi // not recorded//0007030 // Golg
88.62353	110.10694	103.15215	104.191345	NM_001163749//NM_0		0.009	1.16	1.01 Camasp3g	calmodulin regulated spectrin-associated protein family, member 3	0006939 // smooth muscle contraction // inferred from electronic annotation//0007165 // signa
47.30427	37.144222	40.739414	40.724743	NM_031395//NM_1833		0.005	-1.16	-1.00 LOC101055731//LOC1010	synaptotagmin-like protein 3-like//synaptotagmin-like 3	
65.868324	46.16065	49.529713	49.381584	NM_022888//NM_1768		0.007	-1.33	-1.00 Folr4	folate receptor 4 (delta)	
39.2519	31.465635	32.18398	32.061275	NM_0111927		0.010	-1.22	-1.00 Ceaacm9	carcinoembryonic antigen-related cell adhesion molecule 9	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferre
163.18095	227.16814	176.77748	175.95743	NM_026551//XM_0065		0.009	1.08	-1.00 Dcokd	dephospho-CoA kinase domain containing	0005515 // protein binding // inferred from electronic annotation
118.85292	92.06245	100.898254	99.16808	NM_013533//XM_0065		0.009	-1.18	-1.02 Gpr162	G protein-coupled receptor 162	
56.095997	44.037872	46.720684	45.61277	NM_031873		0.003	-1.20	-1.02 Tas1r2	taste receptor, type 1, member 2	0040008 // regulation of growth // inferred from electronic annotation
17355.703	16973.033	17531.281	17099.68	NM_025586//NM_0014		0.007	1.01	-1.03 Gm10224//Gm4581//Gm	predicted pseudogene 10224//predicted gene 4581//ribosomal protein L15	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006352 // DN
2154.2534	1964.3711	2196.0884	2141.9155	NM_009498//XM_0065		0.003	1.02	-1.03 Vamp3	vesicle-associated membrane protein 3	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from
3123.0808	2694.7559	3145.3591	3051.4277	NM_016843		0.008	1.01	-1.03 Atnx10	ataxin 10	0016020 // membrane // inferred from electronic annotation//0016021 // integral component o
32.235867	24.501385	28.645557	27.645136	NM_032397//XM_0065		0.000	-1.13	-1.04 Kcnn1	potassium intermediate/small conductance calcium-activated channel, subfam	0002376 // immune system process // inferred from electronic annotation//0006184 // GTP cata
19.24848	15.291763	18.533731	17.790642	NM_010054		0.000	-1.04	-1.04 Dlx1	distal-less homeobox 2	0007126 // meiotic nuclear division // inferred from electronic annotation//0007283 // spermatc
188.40999	227.36269	234.92706	223.7342	NM_001039084//NM_0		0.009	1.25	-1.05 Mrp1	mitochondrial ribosomal protein L1	0001649 // osteoblast differentiation // inferred from genetic interaction//0001649 // osteoblas
567.57166	621.99115	756.0955	716.8299	NM_010851		0.008	1.33	-1.05 Myd88	myeloid differentiation primary response gene 88	0001938 // positive regulation of endothelial cell proliferation // not recorded//0006935 // cher
889.5055	986.73303	956.73944	903.91754	NM_144904//NM_1781		0.005	1.08	-1.06 Ptpb3	polypyrimidine tract binding protein 3	0006281 // DNA repair // inferred from electronic annotation//0006310 // DNA recombination //
712.7494	759.6339	756.7994	676.767	NM_001039089//NM_0		0.005	1.02	-1.07 Sel1l	sel-1 suppressor of lin-12-like (C. elegans)	0006486 // protein glycosylation // inferred from electronic annotation//0018279 // protein N-li
169.6576	194.38829	241.40405	221.69081	NM_001100449//XM_0		0.006	1.42	-1.09 Taf4b	TAF4B RNA polymerase II, TATA box binding protein (TBP)-associated factor	0000045 // autophagic vacuole assembly // not recorded//0001843 // neural tube closure // infe
90.67312	114.59314	132.84761	121.66651	NM_025782//NM_0272		0.001	1.47	-1.09 Tct39b	tetratricopeptide repeat domain 39B	0000724 // double-strand break repair via homologous recombination // not recorded//0006281
21.2384	21.939253	19.181307	17.497442	NM_020274		0.001	-1.11	-1.10 Htr3b	5-hydroxytryptamine (serotonin) receptor 3B	
94.800545	75.86157	94.42467	85.864525	NM_172794//XM_0065		0.000	1.00	-1.10 Zfp454	zinc finger protein 454	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferre
2079.7288	2153.2583	2137.7793	1942.9963	NM_011051//XM_0065		0.008	1.03	-1.10 Pcd6d	programmed cell death 6	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferre
179.09953	189.35603	185.68564	168.6819	NM_001170953//NM_0		0.009	1.04	-1.10 Rnm1	RNA (guanine-7-) methyltransferase	0016477 // cell migration // inferred from mutant phenotype//0016477 // cell migration // not r
668.83105	688.84827	644.50146	581.3264	NM_031373//XM_0065		0.007	-1.04	-1.11 Ogr1	opioid growth factor receptor	0005576 // extracellular region // inferred from electronic annotation
834.1658	877.58167	778.20465	699.71356	NM_001164156//NM_0		0.000	-1.07	-1.11 Mrcr1	microsphereule protein 1	0016056 // rhodopsin mediated signaling pathway // inferred from mutant phenotype//0043087
66.30488	65.34878	67.65966	59.837852	NM_001013012//XM_0		0.003	1.02	-1.13 Zfp787	zinc finger protein 787	0006468 // protein phosphorylation // inferred from direct assay//0007049 // cell cycle // inferr
95.829056	75.649574	81.587975	72.080086	NM_027010		0.004	-1.17	-1.13 Cyf1	crystallin, gamma F	0019012 // virion // inferred from electronic annotation//0019013 // viral nucleocapsid // infe
695.7521	730.0157	805.5714	710.42755	NM_025693//NR_0377		0.001	1.16	-1.13 Tmem41a	transmembrane protein 41a	0006886 // intracellular protein transport // inferred from electronic annotation//0006887 // ex
525.6154	540.19104	546.61	481.18762	NM_013924		0.008	1.04	-1.14 Abt1	activator of basal transcription 1	0007049 // cell cycle // inferred from electronic annotation//0008283 // cell proliferation // not
101.02462	109.25879	134.81807	118.66679	NM_001081065//XM_0		0.009	1.33	-1.14 Zfp707	zinc finger protein 707	0000041 // retina development in camera-type eye // inferred from mutant phenotype
745.66125	801.71515	847.80945	746.1898	NM_001081394//NM_0		0.001	1.14	-1.14 Tmem248	transmembrane protein 248	0001654 // eye development // inferred from mutant phenotype
1149.6855	1361.4747	1288.8113	1131.5114	NM_025334		0.003	1.12	-1.14 Txnd1c	thioredoxin domain containing 12 (endoplasmic reticulum)	0006611 // protein export from nucleus // inferred from direct assay//0007275 // multicellula c
286.9514	322.07632	359.61365	311.13663	NM_183170		0.008	1.25	-1.16 Mpv17	MPV17 mitochondrial membrane protein-like 2	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein cou
12.404591	14.511468	13.22011	11.371908	NM_001039238//NM_0		0.000	1.07	-1.16 Dcnp1//Dcnp2//Dcnp3	demilune cell and parotid protein 1//demilune cell and parotid protein 2//de	0007275 // multicellular organismal development // inferred from electronic annotation//00160
681.8119	709.64374	832.71295	715.50055	NM_009057//XM_0065		0.004	1.22	-1.16 Scl50a1	solute carrier family 50 (sugar transporter), member 1	
248.0506	270.24194	279.8455	240.37427	NM_029734		0.006	1.13	-1.16 Wdhyh1	WDYHV motif containing 1	0001582 // detection of chemical stimulus involved in sensory perception of sweet taste // not re
115.11313	124.87495	147.29564	125.92162	NM_026117//NM_2076		0.002	1.28	-1.17 Dded2	death effector domain-containing DNA binding protein 2	0006468 // protein phosphorylation // not recorded//0006950 // response to stress // not recor
308.2642	380.97968	343.81018	292.78058	NM_080553//XM_0065		0.009	1.12	-1.17 Itpr3	inositol 1,4,5-triphosphate receptor 3	0001649 // osteoblast differentiation // not recorded//0006397 // mRNA processing // inferred f
33.810482	47.470654	38.702503	32.906536	NM_029360		0.003	1.14	-1.18 Tm4sf3	transmembrane 4 superfamily member 5	
151.4919	120.18614	245.40456	208.30515	NM_001083903//NM_1		0.006	1.62	-1.18 Sbsn	suprabasin	0007275 // multicellular organismal development // inferred from electronic annotation
20.539202	20.808317	21.180328	17.902147	NM_001042418//NM_0		0.010	1.03	-1.18 Cabry	calcium-binding tyrosine-(Y)-phosphorylation regulated (fibrousheathin 2)	0007275 // multicellular organismal development // inferred from electronic annotation
1980.7354	1968.3641	1996.457	1682.3652	NM_001199274//NM_1		0.004	1.01	-1.19 Mat2b	methionine adenosyltransferase II, beta	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // reg
983.54016	1002.24927	1031.7991	861.6388	NM_145606		0.003	1.05	-1.20 Chmp1a	charged multivesicular body protein 1A	0031069 // hair follicle morphogenesis // inferred from mutant phenotype
1007.682	1060.9253	854.2852	711.68445	NM_025915		0.009	-1.18	-1.20 Tmem58	transmembrane protein 58	0006457 // protein folding // inferred from direct assay//0006662 // glycerol ether metabolic pr
112.45588	106.81234	128.25092	106.510216	NM_172875//XM_0065		0.007	1.14	-1.20 Aizin2	antizyme inhibitor 2	0007565 // female pregnancy // inferred from electronic annotation
1369.2303	1433.6484	1616.869	1333.6819	NM_001199009//NM_1		0.009	1.18	-1.21 Dcpl11	DBP1 and CUL4 associated factor 11	0032259 // methylation // inferred from electronic annotation
270.13675	307.58252	340.55954	280.72928	NM_001004190		0.004	1.26	-1.21 Zfp560	zinc finger protein 560	0000226 // microtubule cytoskeleton organization // inferred from direct assay//0006184 // GTP
924.38574	939.7349	906.2641	737.0504	NM_001199004//NM_0		0.007	-1.02	-1.23 Gola5	golgi autoantigen, golgin subfamily a, 5	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // reg
350.96143	360.64636	407.9188	327.77188	NM_013770		0.005	1.16	-1.24 Sc15a10	solute carrier family 25 (mitochondrial carrier, dicarboxylate transporter), mem	0000070 // mitotic sister chromatid segregation // inferred from mutant phenotype//0007049 //
239.12836	276.19635	247.31636	196.78394	NM_133733//XM_0065		0.005	1.03	-1.26 Clmp	CXADR-like membrane protein	0005537 // mannose binding // inferred from direct assay//0030246 // carbohydrate binding // i
924.40405	916.7021	981.994	779.34906	NM_029354//XM_0065		0.007	1.06	-1.26 Mzt2	mitotic spindle organizing protein 2	
109.7685	105.43333	129.01692	102.36427	NM_001164567//NM_0		0.005	1.18	-1.26 Vill	villin-like	0035418 // protein localization to synapse // inferred from mutant phenotype
34.793518	34.548595	33.996597	26.567661	NM_001285482//NM_0		0.008	-1.02	-1.28 Htr1d	5-hydroxytryptamine (serotonin) receptor 1D	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // reg
4619.4604	4740.4546	9125.774	7125.0015	NM_007801		0.008	1.98	-1.28 Ctsb	cathepsin H	0008544 // epidermis development // inferred from electronic annotation
4124.035	4033.8813	4911.382	3813.3694	NM_007657		0.009	1.19	-1.29 Cd9	CD9 antigen	0006508 // proteolysis // inferred from electronic annotation//0006749 // glutathione metabolic
58.654034	66.26042	57.22359	44.23415	NR_040406//NR_04040		0.007	-1.02	-1.29 Gm16845	predicted gene, 16845	0008152 // metabolic process // not recorded//0051586 // positive regulation of dopamine upa
94.84323	114.48559	238.80887	184.10858	NM_009897//XM_0064		0.003	2.52	-1.30 Kmt1	creatine kinase, mitochondrial 1, ubiquitous	0006898 // receptor-mediated endocytosis // not recorded//0006935 // chemotaxis // inferred f
160.46207	220.5536	441.01245	337.7131	NM_001083894//NM_0		0.005	2.75	-1.31 Liph	lipase, member H	0008277 // regulation of G-protein coupled receptor protein signaling pathway // inferred from g
121.60832	182.8558	214.94002	164.22755	NM_028009//XM_0065		0.006	1.01	-1.31 Rpsud1	RNA pseudouridylation synthase domain containing 1	
103.562805	122.44802	153.63472	115.27902	NM_001082975//XM_0		0.007	1.48	-1.33 Sdr39u1	short chain dehydrogenase/reductase family 39U, member 1	0007155 // cell adhesion // inferred from mutant phenotype//0007338 // single fertilization // in
609.43494	616.3825	585.8399	433.93536	NM_001270495//NM_0		0.003	-1.04	-1.35 Tmem254a//Tmem254b	transmembrane protein 254a//transmembrane protein 254b//transmembran	0006590 // thyroid hormone generation // not recorded//0009409 // response to cold // not rec
500.6313	546.75055	652.7005	476.94382	NM_011611//NM_1707		0.006	1.30	-1.37 Cd40	CD40 antigen	0007155 // cell adhesion // inferred from electronic annotation//0008285 // negative regulati
247.25008	274.07913	330.198	239.52315	NM_001243584//NM_0		0.005	1.34	-1.38 Mif4gd	MIF4G domain containing	0006810 // transport // inferred from electronic annotation//0015031 // protein transport // inh
184.00974	175.80466	252.7704	182.76837	NM_001286038//NM_0		0.009	1.37	-1.38 Klc3	kinesin light chain 3	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferre
1144.5792	1152.8401	1104.2269	796.5783	NM_001270495//NM_0		0.004	-1.04	-1.39 Tmem254a//Tmem254b	transmembrane protein 254a//transmembrane protein 254b//transmembran	0001764 // neuron migration // inferred from electronic annotation//0006184 // GTP catalyti
3097.0762	2950.8845	3751.1406	2688.6208	NM_010261		0.005	1.21	-1.40 Rabac1	Rab acceptor 1 (prenylated)	0005737 // cytoplasm // inferred from electronic annotation//0005856 // cytoskeleton // inferre
59.049698	52.857567	55.86813	39.78884	NM_027622		0.006	-1.06	-1.40 Txs19.2	testis expressed gene 19.2	0009922 // spindle pole // not recorded//0005737 // cytoplasm // not recorded//0005814 // ce
1979.6515	1891.6511	2086.9712	1478.3418	NM_009101//XM_0065		0.002	1.05	-1.41 Rras	Harvey rat sarcoma oncogene, subgroup R	0010468 // regulation of gene expression // not recorded//0030154 // cell differentiation // infe
90.2437	104.66821	185.40825	127.885994	NM_175638//XM_0065		0.007	2.05	-1.45 Wnk4	WNK lysine deficient protein kinase 4	
81.064354	73.11081	82.32966	54.972485	NM_001007582		0.000	1.00	-1.50 AYT61184	cDNA sequence AY761184	
4887.4385	4920.806	9818.816	6502.976	NM_011313		0.010	2.01	-1.51 S100a6	S100 calcium binding protein A6 (calcylin)	0001525 // angiogenesis // inferred from electronic annotation//0007155 // cell adhesion // infe
923.67535	903.7491	1084.5637	705.1583	NM_010579		0				

[ICR, Air, PBS][ICR, Air, SFN [ICR, O2, PBS][ICR, O2, SFN][RefSeq Transcript ID				p (Prenatal Treatment-Exposure)	FC [Air-PBS: O2-PBS FC [O2 PBS:SFN]Gene Symbol	Gene Title	Gene Ontology
1985.1251	2506.2043	2176.9446	934.4288 NM_001267808	0.004	1.10	-2.33 H2-D1	// cell cycle // inferred from electronic annotation
1195.5133	1377.2422	5246.056	1710.0326 NM_008491	0.001	4.39	-3.07 Lcn2	// mitotic nuclear division

[illegible]

[Nrf2-KO, Air, PBS][r [Nrf2-KO, Air, SFN]] [Nrf2-KO, O2, PBS]] [Nrf2-KO, O2, SFN]] [RefSeq Transcript ID p (Prenatal Treatment-Exposure)				FC [Air-PBS:O2-PBS]	FC [O2 PBS:SFN]	Gene Symbol	Gene Title	Gene Ontology
102.074425	143.36925	415.62582	165.67465 NM_001081205	0.009	4.07	-2.51 Nipa1l	NIPA-like domain containing 1	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//00:
558.2761	815.70386	2517.2708	907.5686 NM_020008	0.001	4.51	-2.77 Clec7a	C-type lectin domain family 7, member a	0001878 // response to yeast // inferred from direct assay//0001879 // detection of yeast // inferred from direct assay//0002221

Table S5. Prenatal sulforaphane-modulated genes in *Nrf2*^{+/+} placenta (T Test unpaired p-value P <= 0.05).

>=1.5-fold 708 genes

RIKEN cDNA and predicted genes excluded. Fold Change (FC): Blue (-) - fold lower in SFN than PBS, Red - fold higher in SFN than PBS.

[ICR, PBS]	[ICR, SUL]	p	RefSeq Transcript ID	FC [PBS:SFN]	Gene Symbol	Gene Title	Gene Ontology Biological Process
35.40988	266.3408	0.005	NM_025288	7.33	<i>Stfa3</i>	stefin A3	0004869 // cysteine-type endopeptidase inhibitor activity // inferred from electronic annotation
112.3694	554.5562	0.009	NM_001082543///NM	4.56	<i>BC100530//Stfa1</i>	cDNA sequence BC100530//stefin A1	0004869 // cysteine-type endopeptidase inhibitor activity // inferred from electronic annotation
94.05842	412.6405	0.011	NM_026516	4.33	<i>Tmem178</i>	transmembrane protein 178	0005198 // structural molecule activity // inferred from electronic annotation
24.77076	87.45144	0.042	NM_011670	3.69	<i>Uchl1</i>	ubiquitin carboxy-terminal hydrolase L1	0007409 // axonogenesis // inferred from mutant phenotype//0019896 // axon transport of mi
77.77694	255.1708	0.011	NM_144848	3.26	<i>Eppk1</i>	epiplakin 1	0005737 // cytoplasm // inferred from direct assay//0005856 // cytoskeleton // inferred from e
43.68089	148.7498	0.040	NM_010441	3.10	<i>Hmg2</i>	high mobility group AT-hook 2	0051301 // cell division // inferred from electronic annotation//0007049 // cell cycle // inferrec
11.32679	35.95194	0.012	NM_027137	3.04	<i>Lce1d</i>	late cornified envelope 1D	
41.48204	109.7844	0.035	NM_199473	2.92	<i>Col8a2</i>	collagen, type VIII, alpha 2	0048593 // camera-type eye morphogenesis // inferred from genetic interaction//0007155 // c
211.6307	621.1341	0.018	NM_009209	2.88	<i>Slc6a2</i>	solute carrier family 6 (neurotransmitter transporter, noradrenalin), mem	0015844 // monoamine transport // not recorded//0015874 // norepinephrine transport // infi
92.00953	256.2665	0.018	NM_011485	2.87	<i>Star</i>	steroidogenic acute regulatory protein	0044255 // cellular lipid metabolic process // inferred from mutant phenotype//0010288 // res
426.3177	1176.62	0.028	NM_007406///NM_0	2.86	<i>Adcy7</i>	adenylate cyclase 7	0009190 // cyclic nucleotide biosynthetic process // inferred from electronic annotation//00006
95.5387	257.2281	0.009	NM_001081139	2.80	<i>Ankrd35</i>	ankyrin repeat domain 35	
349.9298	911.0887	0.028	NM_001081362	2.79	<i>Trapp</i>	transformation/transcription domain-associated protein	0016568 // chromatin modification // inferred from electronic annotation//0006355 // regulati
44.18663	110.3886	0.046	NM_008508	2.77	<i>Lor</i>	loricrin//Loricrin, mRNA (cDNA clone IMAGE:4190845)	0030216 // keratinocyte differentiation // inferred from electronic annotation//0031424 // ker:
357.6803	1011.711	0.014	NM_033314	2.76	<i>Slco2a1</i>	solute carrier organic anion transporter family, member 2a1//Solute carri	0015732 // prostaglandin transport // inferred from direct assay//0006810 // transport // infer
209.9585	566.8061	0.012	NM_177386	2.75	<i>Sfmbt2</i>	Scm-like with four mbt domains 2	0045449 // regulation of transcription // inferred from electronic annotation
211.0596	604.8945	0.018	XM_001476334///XM	2.75	<i>100042151//1000432</i>	predicted gene, 100039204//hypothetical protein LOC100047648//CWC:	0008380 // RNA splicing // inferred from electronic annotation//0006397 // mRNA processing /
24.54087	68.3346	0.024	NM_025984	2.71	<i>Lce1a1</i>	late cornified envelope 1A1	
489.1765	1312.866	0.019	NM_007984	2.66	<i>Fscn1</i>	fascin homolog 1, actin bundling protein (Strongylocentrotus purpuratus)	0003779 // actin binding // inferred from electronic annotation//0003779 // actin binding // int
196.8718	467.3081	0.044	NM_001081098	2.59	<i>Zfp362</i>	zinc finger protein 362	0008270 // zinc ion binding // inferred from electronic annotation//0003676 // nucleic acid bin
930.6491	2130.405	0.045	NM_001146268///NM	2.57	<i>Pdgfrb</i>	platelet derived growth factor receptor, beta polypeptide	0008284 // positive regulation of cell proliferation // inferred from electronic annotation//00006
118.9973	282.2134	0.022	NM_001109661///NM	2.52	<i>Bach2</i>	BTB and CNC homology 2	0006355 // regulation of transcription, DNA-dependent // inferred from direct assay//0006355
161.0767	377.9266	0.030	NM_007872///NM_1	2.51	<i>Dnmt3a</i>	DNA methyltransferase 3A	0007283 // spermatogenesis // inferred from mutant phenotype//0006346 // methylation-dep
74.91989	179.8726	0.008	NM_010101	2.51	<i>S1pr3</i>	sphingosine-1-phosphate receptor 3	0007165 // signal transduction // inferred from electronic annotation//0032651 // regulation o
61.43885	149.0868	0.023	NM_001081417	2.51	<i>Chd7</i>	chromodomain helicase DNA binding protein 7	0030540 // female genitalia development // inferred from mutant phenotype//0042472 // inne
188.5176	481.9748	0.016	XM_001476334///XM	2.50	<i>100042151//1000432</i>	predicted gene, 100039204//hypothetical protein LOC100047648//CWC:	0008380 // RNA splicing // inferred from electronic annotation//0006397 // mRNA processing /
282.5281	640.1924	0.038	NM_001081109	2.48	<i>Lmtk2</i>	lemur tyrosine kinase 2	0007399 // nervous system development // not recorded//0048011 // nerve growth factor rec
23.55192	57.13178	0.002	NM_009144	2.44	<i>Sfrp2</i>	secreted frizzled-related protein 2	0007275 // multicellular organismal development // inferred from electronic annotation//0030
174.2613	389.5284	0.037	NM_010800	2.42	<i>Bhlha15</i>	basic helix-loop-helix family, member a15	0048469 // cell maturation // inferred from mutant phenotype//0006851 // mitochondrial calc
313.2889	726.1153	0.016	NM_027373	2.40	<i>Afap1</i>	actin filament associated protein 1	0009966 // regulation of signal transduction // not recorded
199.5643	458.1648	0.011	NM_001081279	2.37	<i>Mfh3a1</i>	malignant fibrous histiocytoma amplified sequence 1	0005515 // protein binding // inferred from electronic annotation
44.1906	106.9033	0.044	NM_008725	2.35	<i>Nppa</i>	natriuretic peptide precursor type A	0050880 // regulation of blood vessel size // inferred from electronic annotation//0008217 // r
422.2918	971.3632	0.010	NM_175451	2.31	<i>Kkap4</i>	cytoskeleton-associated protein 4	0005515 // protein binding // not recorded
50.9815	123.5872	0.046	NM_021285///NM_0	2.28	<i>Myl1</i>	myosin, light polypeptide 1	0003774 // motor activity // inferred from electronic annotation//0005509 // calcium ion bindi
417.8607	906.8631	0.040	NM_175260	2.25	<i>Myh10</i>	myosin, heavy polypeptide 10, non-muscle//Myosin, heavy polypeptide 1	0021678 // third ventricle development // inferred from mutant phenotype//0007097 // nucle:
480.0858	1007.058	0.031	NM_001083935///NM	2.25	<i>Pth1r</i>	parathyroid hormone 1 receptor	0002076 // osteoblast development // inferred from mutant phenotype//0048469 // cell matu
72.74856	153.3457	0.048	NM_978355///XM_9C	2.23	<i>Klhl29</i>	kelch-like 29 (Drosophila)	0005515 // protein binding // inferred from electronic annotation
118.6122	260.5463	0.004	NM_011941	2.23	<i>Mapkbp1</i>	mitogen-activated protein kinase binding protein 1	0007256 // activation of JNKK activity // inferred from direct assay
161.7701	366.8025	0.012	NM_133833///NM_1	2.22	<i>Dst</i>	dystonin	0031122 // cytoplasmic microtubule organization // inferred from mutant phenotype//000809
146.2006	316.1447	0.002	NM_001160268///NM	2.21	<i>Plekha6</i>	pleckstrin homology domain containing, family A member 6	
133.2459	271.5109	0.046	NM_011214///NM_0	2.19	<i>Ptpnru</i>	protein tyrosine phosphatase, receptor type, U	0034109 // homotypic cell-cell adhesion // inferred from direct assay//0016311 // dephosphor
205.0009	421.9397	0.028	NM_001025379	2.19	<i>Sema3g</i>	sema domain, immunoglobulin domain (Ig), short basic domain, secreted,	0007275 // multicellular organismal development // inferred from electronic annotation
53.65535	115.8217	0.004	NM_011976	2.19	<i>Sema4g</i>	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM)	0007275 // multicellular organismal development // inferred from electronic annotation//0030
1618.126	3295.512	0.039	NM_009932	2.17	<i>Col4a2</i>	collagen, type IV, alpha 2	0016525 // negative regulation of angiogenesis // inferred from sequence or structural similarity
253.4368	521.8038	0.036	NM_015734	2.15	<i>Col5a1</i>	collagen, type V, alpha 1	0007155 // cell adhesion // inferred from electronic annotation//0051128 // regulation of cellu
423.3071	888.5441	0.037	NM_016710	2.15	<i>Nsfp1</i>	nucleosome binding protein 1	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation//
1094.84	2244.811	0.034	XM_621314///NM_0:	2.14	<i>Dsp</i>	desmoplakin	0016323 // basolateral plasma membrane // inferred from direct assay//0030057 // desmosom
51.63446	106.1434	0.020	NM_177047	2.14	<i>Auts2</i>	Autism susceptibility candidate 2, mRNA (cDNA clone IMAGE:5347232)//autism susceptibility candidate 2	0007264 // small GTPase mediated signal transduction // inferred from electronic annotation//
380.7839	772.0258	0.023	NM_001039677	2.12	<i>Slc30a2</i>	solute carrier family 30 (zinc transporter), member 2	0006812 // cation transport // inferred from electronic annotation
963.4966	1955.262	0.029	NM_001113488///NM	2.11	<i>9-Sep</i>	septin 9	0051301 // cell division // inferred from electronic annotation//0007049 // cell cycle // inferrec
59.62911	120.9713	0.014	NM_178660	2.11	<i>Rbms3</i>	RNA binding motif, single stranded interacting protein	0003723 // RNA binding // inferred from electronic annotation//0000166 // nucleotide binding
177.435	377.6742	0.018	NM_173036	2.11	<i>Gpr97</i>	G protein-coupled receptor 97	0007165 // signal transduction // inferred from electronic annotation//0007218 // neuropeptid
161.2454	318.297	0.044	NM_172493///NM_0	2.11	<i>Diap2</i>	diaphanous homolog 2 (Drosophila)	0030036 // actin cytoskeleton organization // inferred from electronic annotation//0007275 //
545.8066	1091.028	0.034	NM_009059	2.11	<i>Rgl2</i>	ral guanine nucleotide dissociation stimulator-like 2	0007264 // small GTPase mediated signal transduction // inferred from electronic annotation//
100.7942	195.8783	0.048	NM_021366	2.10	<i>Klf13</i>	Kruppel-like factor 13 (Klf13), mRNA//Kruppel-like factor 13	0006366 // transcription from RNA polymerase II promoter // inferred from sequence or structu
18.04456	37.9812	0.010	XM_001474909///XM	2.10	<i>Tnik</i>	TRAF2 and NCK interacting kinase, mRNA (cDNA clone MGC:183916 IMAGE:0006950)	0006950 // response to stress // inferred from sequence or structural similarity//0007243 // pr
191.2534	402.5042	0.018	NM_153396///XM_9:	2.09	<i>Mical3</i>	microtubule associated monooxygenase, calponin and LIM domain containin	0008152 // metabolic process // inferred from electronic annotation

[ICR, PBS]([ICR, SUL])p	RefSeq Transcript ID	FC [PBS:SFN]	Gene Symbol	Gene Title	Gene Ontology Biological Process
118.5959 240.8447	0.008 NM_001040398	2.07	Setd1b	SET domain containing 1B	0016568 // chromatin modification // inferred from electronic annotation///0006355 // regulati
291.136 591.001	0.007 NM_175155	2.07	Sash1	SAM and SH3 domain containing 1	0007049 // cell cycle // inferred from electronic annotation///0045786 // negative regulation of
626.7794 1221.173	0.042 NM_001040459	2.06	Shroom4	shroom family member 4	0007275 // multicellular organismal development // inferred from electronic annotation///0007
176.0527 349.1648	0.017 NM_172457	2.06	Mobkl2a	MOB1, Mps One Binder kinase activator-like 2A (yeast)	0005515 // protein binding // inferred from electronic annotation///0046872 // metal ion bindir
9.943523 20.63494	0.009 NR_001586///NM_0C	2.06	Speer1-ps1///EG54572	spermatogenesis associated glutamate (E)-rich protein 1, pseudogene 1///predicted gene, EG545728///predicted gene, EG623898	
132.4335 282.453	0.041 NM_029667	2.06	Lce1i	late cornified envelope 1l	
521.2607 1072.452	0.012 NM_001033380	2.05	Itpril2	inositol 1,4,5-triphosphate receptor interacting protein-like 2	0016021 // integral to membrane // inferred from electronic annotation///0016020 // membrar
174.54 345.2822	0.028 NM_015830	2.05	Solh	Mus musculus, clone IMAGE:4241884///small optic lobes homolog (Drosophila)	0006508 // proteolysis // inferred from electronic annotation
169.1234 323.1221	0.044 NM_001113573///NM	2.05	Brd3	bromodomain containing 3	0005634 // nucleus // inferred from electronic annotation
447.3822 873.7873	0.042 NM_172397	2.03	Limd2	LIM domain containing 2	0046872 // metal ion binding // inferred from electronic annotation///0008270 // zinc ion bindir
972.4028 1925.166	0.009 NM_025294	2.02	Gtlf3b	gene trap locus F3b	
169.0003 332.5705	0.017 NM_010683	2.02	Lamc1	laminin, gamma 1	0022617 // extracellular matrix disassembly // inferred from electronic annotation///0016477 //
337.8081 641.7703	0.037 NM_020508///XM_0I	2.02	Brd4	bromodomain containing 4	0043388 // positive regulation of DNA binding // inferred from direct assay///0006468 // protei
230.9898 458.0944	0.034 NM_013807	2.02	Plk3	polo-like kinase 3 (Drosophila)	0007049 // cell cycle // inferred from electronic annotation///0006468 // protein amino acid ph
46.18642 93.42761	0.026	2.01	D15Wsu126e	DNA segment, Chr 15, Wayne State University 126, expressed	
145.1635 285.2369	0.038 NM_201385///NM_2	2.00	LOC671535///Plec1	similar to Plec1 protein///plectin 1	0003779 // actin binding // inferred from electronic annotation///0003950 // NAD+ ADP-ribosyl
376.4715 746.1816	0.033 NM_009362	2.00	Tff1	trefoil factor 1	0030154 // cell differentiation // inferred from mutant phenotype///0009611 // response to wo
238.0372 449.8092	0.037 NM_172827	2.00	Lnpep	leucyl/cystinyl aminopeptidase	0030147 // natriuresis // inferred from electronic annotation///0048169 // regulation of long-te
157.7969 301.0559	0.034 NM_001042623///NM	1.99	Phc1	polyhomeotic-like 1 (Drosophila)	0007275 // multicellular organismal development // inferred from electronic annotation
232.68 443.4164	0.026 NM_001081118	1.99	Phrf1	PHD and ring finger domains 1	0006366 // transcription from RNA polymerase II promoter // not recorded///0007242 // intrac
164.3662 321.0152	0.029 NM_177409///NM_1	1.99	Tram2	translocating chain-associating membrane protein 2	0050002 // intracellular protein transmembrane transport // inferred from electronic annotation
2025.212 3853.207	0.034 NM_010137///XM_0I	1.98	LOC100048537///Epa6	endothelial PAS domain protein 1///similar to Endothelial PAS domain prot	0043129 // surfactant homeostasis // inferred from mutant phenotype///0007275 // multicellul
133.997 252.9343	0.026 NM_001024955///NM	1.97	Pik3r1	phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 1 (p85 alpha)	0007165 // signal transduction // inferred from electronic annotation///0048009 // insulin-like g
66.61494 128.0928	0.027 NM_199068	1.97	Foxk1	forkhead box K1	0007275 // multicellular organismal development // inferred from electronic annotation///0045
722.7357 1335.036	0.049 NM_013605	1.97	Muc1	mucin 1, transmembrane	0016324 // apical plasma membrane // inferred from direct assay///0005634 // nucleus // inferi
134.2631 251.8326	0.040 NM_172882	1.96	Wdfy3	WD repeat and FYVE domain containing 3	0016757 // transferase activity, transferring glycosyl groups // inferred from electronic annotati
188.671 360.7327	0.017 NM_016808///NM_1	1.96	Usp2	ubiquitin specific peptidase 2	0019941 // modification-dependent protein catabolic process // inferred from electronic annota
62.10377 118.003	0.020 NM_027011	1.96	Krt5	keratin 5	0005198 // structural molecule activity // inferred from electronic annotation///0005515 // prot
198.6434 373.9885	0.030 NM_019472	1.95	Myo10	myosin X	0007165 // signal transduction // inferred from electronic annotation
203.4426 396.5453	0.024 NM_001145836///NM	1.95	Ralgds	ral guanine nucleotide dissociation stimulator	0007264 // small GTPase mediated signal transduction // inferred from electronic annotation///
171.969 325.3518	0.016 NM_173760	1.95	Hisppd1	histidine acid phosphatase domain containing 1	0006020 // inositol metabolic process // inferred from sequence or structural similarity
574.0403 1082.442	0.032 NM_011597	1.95	Tjp2	tight junction protein 2	0005515 // protein binding // inferred from electronic annotation///0005515 // protein binding
668.043 1290.094	0.017 NM_007883	1.94	Dsg2	desmoglein 2///Desmoglein 2 (Dsg2), mRNA	0007156 // homophilic cell adhesion // inferred from electronic annotation///0007155 // cell ad
470.3322 870.0803	0.036 NM_011962	1.94	Plod3	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3	0019538 // protein metabolic process // inferred from electronic annotation///00055114 // oxida
37.30195 71.44573	0.012 NM_011256	1.94	Pitpnm2	phosphatidylinositol transfer protein, membrane-associated 2	0006810 // transport // inferred from electronic annotation
89.97656 173.5232	0.023 NM_008641///NM_0	1.94	Mast2	microtubule associated serine/threonine kinase 2///Microtubule associate	0048515 // spermatid differentiation // inferred from direct assay///0006468 // protein amino a
104.7456 195.4346	0.030 NM_198109	1.93	Ssh1	slingshot homolog 1 (Drosophila)	0016311 // dephosphorylation // inferred from electronic annotation///0006470 // protein amir
56.81121 110.8075	0.033 NM_178406	1.92	Gpr153	G protein-coupled receptor 153	0007165 // signal transduction // inferred from electronic annotation///0007186 // G-protein cc
193.6991 361.0289	0.021 NM_173379	1.92	Leprel1	leprecan-like 1	0019538 // protein metabolic process // inferred from electronic annotation///00055114 // oxida
516.5957 971.8157	0.020 NM_139140	1.92	Spats2	spermatogenesis associated, serine-rich 2	0005737 // cytoplasm // inferred from direct assay///0005737 // cytoplasm // inferred from ele
116.0436 219.221	0.024 NM_172424	1.92	Med13l	mediator complex subunit 13-like	0006357 // regulation of transcription from RNA polymerase II promoter // inferred from electr
658.4739 1220.883	0.028 NM_175414	1.92	Tspan9	tetraspanin 9	0016021 // integral to membrane // inferred from electronic annotation///0016020 // membrar
75.09846 139.9092	0.025 NM_018775	1.91	Tbc1d8	TBC1 domain family, member 8	0032313 // regulation of Rab GTPase activity // inferred from electronic annotation
504.3522 951.1658	0.006 NM_133626///NM_0	1.91	Rrbp1	ribosome binding protein 1	0065002 // intracellular protein transmembrane transport // inferred from electronic annotati
275.4002 519.4771	0.037 NM_144925	1.91	Tnrc6a	trinucleotide repeat containing 6a	0009267 // cellular response to starvation // inferred from direct assay///0032507 // mainten
166.5425 311.159	0.010 NM_009686	1.90	Apbb2	amyloid beta (A4) precursor protein-binding, family B, member 2	0030308 // negative regulation of cell growth // inferred from direct assay///0030048 // actin fil
221.0302 412.165	0.008 NM_007842	1.90	Dhx9	DEAH (Asp-Glu-Ala-His) box polypeptide 9	0034605 // cellular response to heat // inferred from direct assay
113.2601 209.0205	0.021 NM_010221	1.90	Fkbp10	FK506 binding protein 10	0006457 // protein folding // inferred from electronic annotation
198.865 373.955	0.036 NM_011866	1.90	Pde10a	phosphodiesterase 10A	0045672 // positive regulation of osteoclast differentiation // inferred from mutant phenotype/
220.3442 413.3039	0.014 NM_001081337	1.89	Sipa1l2	signal-induced proliferation-associated 1 like 2	0051056 // regulation of small GTPase mediated signal transduction // inferred from electronic
104.6065 196.355	0.036 NM_007403	1.89	Adam8	a disintegrin and metallopeptidase domain 8	0007229 // integrin-mediated signaling pathway // inferred from electronic annotation///00065
90.01758 164.9848	0.033 NM_011104	1.89	Prkce	protein kinase C, epsilon	0007635 // chemosensory behavior // traceable author statement///0007242 // intracellular sig
18.21033 34.43372	0.014 NM_181540	1.89	Tm6sf2	transmembrane 6 superfamily member 2	0016021 // integral to membrane // inferred from electronic annotation///0016020 // membrar
239.9004 446.5806	0.037 NM_178661	1.88	Creb3l2	cAMP responsive element binding protein 3-like 2	0006986 // response to unfolded protein // inferred from electronic annotation///0006355 // re
2881.238 5221.864	0.020 NM_009931	1.88	Col4a1	collagen, type IV, alpha 1	0005201 // extracellular matrix structural constituent // inferred from electronic annotation///0
152.6381 274.8745	0.032 NM_001122676///NM	1.88	Zcchc2	zinc finger, CCHC domain containing 2///Zinc finger, CCHC domain containi	0007154 // cell communication // inferred from electronic annotation
1230.772 2225.907	0.024 NM_013676	1.87	Supt5h	suppressor of Ty 5 homolog (S. cerevisiae)	0006357 // regulation of transcription from RNA polymerase II promoter // inferred from electr
24.47387 44.5047	0.012 NM_146061	1.87	Prr5	proline rich 5 (renal)	0007049 // cell cycle // inferred from electronic annotation///0030335 // positive regulation of
32.2329 59.10203	0.023 NM_173368	1.87	Chd6	chromodomain helicase DNA binding protein 6	0006333 // chromatin assembly or disassembly // inferred from electronic annotation
110.2013 203.1034	0.012 NM_146030	1.87	Plekhh3	pleckstrin homology domain containing, family H (with MyTH4 domain) me	0007165 // signal transduction // inferred from electronic annotation

[ICR, PBS]([ICR, SUL])p	RefSeq Transcript ID	FC [PBS:SFN]	Gene Symbol	Gene Title	Gene Ontology Biological Process
447.5739 820.1391	0.025 NM_016747	1.87	Dlg3	discs, large homolog 3 (Drosophila)	0005515 // protein binding // inferred from electronic annotation///0005515 // protein binding
106.0816 189.2577	0.033 NM_013495	1.87	Cpt1a	carnitine palmitoyltransferase 1a, liver	0042755 // eating behavior // inferred from electronic annotation///0006810 // transport // inf
107.5898 197.2989	0.019 NM_010700	1.87	Ldlr	low density lipoprotein receptor	0008202 // steroid metabolic process // inferred from electronic annotation///0008203 // chole
71.08664 127.684	0.036 NM_197940	1.87	Wipf2	WAS/WASL interacting protein family, member 2	0003779 // actin binding // inferred from electronic annotation
8715.003 15611.46	0.046 NM_011120	1.86	Prl7d1	prolactin family 7, subfamily d, member 1	0043537 // negative regulation of blood vessel endothelial cell migration // inferred from direct
85.80798 152.241	0.039 NM_181072	1.86	Myo1e	myosin IE	0006807 // nitrogen compound metabolic process // inferred from mutant phenotype///000182
295.6276 532.4476	0.019 NM_144922///NM_1	1.86	Hnnpul1	heterogeneous nuclear ribonucleoprotein U-like 1	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation//
225.7229 409.9263	0.014 NM_010153	1.86	ErbB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	0043524 // negative regulation of neuron apoptosis // inferred from mutant phenotype///00075
428.554 751.7423	0.046 NM_023598///XM_0i	1.86	LOC100044968///Arid1	similar to modulator recognition factor 2///AT rich interactive domain 5B	0060021 // palate development // inferred from mutant phenotype///0060325 // face morphog
111.322 208.9804	0.024 XM_001478845///NN	1.85	5830417110Rik///LOC6	similar to Dingo protein isoform 2///RIKEN cDNA 5830417110 gene	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation
322.5857 596.9042	0.011 NM_010501	1.85	Ilf1t3	interferon-induced protein with tetratricopeptide repeats 3	0005488 // binding // inferred from electronic annotation
19.1484 35.43503	0.018 XM_001478962///XM	1.85	Muc3	mucin 3, intestinal	0016324 // apical plasma membrane // inferred from direct assay
58.71035 106.2942	0.025 NM_175268///NM_2	1.84	Fam53b	family with sequence similarity 53, member B	
307.8058 567.5307	0.024 NM_177461	1.84	Mical1	microtubule associated monooxygenase, calponin and LIM domain containin	0005856 // cytoskeleton // inferred from electronic annotation///0005737 // cytoplasm // inferi
665.9888 1232.495	0.015 NM_172588	1.84	Serinc5	serine incorporator 5	0006658 // phosphatidylserine metabolic process // inferred from sequence or structural similar
1613.667 2866.976	0.046 NM_001093766///NN	1.83	Myadim	myeloid-associated differentiation marker	0016021 // integral to membrane // inferred from electronic annotation///0016020 // membrar
35.24829 62.94902	0.011 XM_001476544///XM	1.83	Ttc28	tetratricopeptide repeat domain 28	0005488 // binding // inferred from electronic annotation
787.5598 1384.153	0.047 NM_139149	1.82	Fus	fusion, derived from t(12;16) malignant liposarcoma (human)	0045944 // positive regulation of transcription from RNA polymerase II promoter // inferred from
131.4118 236.1165	0.038 NM_080448	1.81	Srgap3	SLIT-ROBO Rho GTPase activating protein 3	0007165 // signal transduction // inferred from electronic annotation
79.89884 139.4792	0.025 NM_010513	1.81	Igf1r	insulin-like growth factor I receptor	0048009 // insulin-like growth factor receptor signaling pathway // inferred from sequence or st
750.2532 1312.093	0.023 NM_198703	1.81	Wnk1	WNK lysine deficient protein kinase 1	0032776 // DNA methylation on cytosine // inferred from electronic annotation///0006468 // pr
67.28961 118.5715	0.030 NM_011929	1.81	Clcn6	chloride channel 6	0006821 // chloride transport // inferred from electronic annotation///0006811 // ion transport
58.44442 104.9145	0.022 NM_011345	1.80	Sele	selectin, endothelial cell	0007155 // cell adhesion // inferred from electronic annotation
122.1599 212.6065	0.036 NM_001025395///NM	1.80	Src	Rous sarcoma oncogene	0006950 // response to stress // inferred from electronic annotation///0018108 // peptidyl-tyro
316.7528 550.055	0.031 NM_0011202///NM_0	1.80	Ptpn11	protein tyrosine phosphatase, non-receptor type 11	0007409 // axonogenesis // inferred from mutant phenotype///0016311 // dephosphorylation //
324.0155 569.0248	0.011 NM_020006	1.80	Cdc42ep4	CDC42 effector protein (Rho GTPase binding) 4	0031274 // positive regulation of pseudopodium assembly // inferred from electronic annotatio
356.1224 635.7925	0.021 NM_178612	1.80	Cnpy4	canopy 4 homolog (zebrafish)	0032880 // regulation of protein localization // not recorded
121.4798 210.217	0.026 NM_007997	1.79	Fdxr	ferredoxin reductase	0008202 // steroid metabolic process // inferred from electronic annotation///0055114 // oxida
860.3024 1502.002	0.022 NM_030887	1.79	Jdp2	Jun dimerization protein 2	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation//
197.5953 338.5231	0.040 NM_011385	1.79	Ski	ski sarcoma viral oncogene homolog (avian)	0030326 // embryonic limb morphogenesis // inferred from mutant phenotype
134.4079 240.2669	0.033 NM_001017426	1.79	Kdm6b	KDM1 lysine (K)-specific demethylase 6B///Jumonji domain containing 3, n	0016568 // chromatin modification // inferred from electronic annotation///0055114 // oxidati
256.6292 453.266	0.027 NM_022995	1.79	Pmepa1	prostate transmembrane protein, androgen induced 1	0005515 // protein binding // inferred from physical interaction
152.4786 261.2643	0.041 NM_001080819	1.79	Arid1a	AT rich interactive domain 1A (SWI-like)	0030520 // estrogen receptor signaling pathway // inferred from sequence or structural similarit
128.4421 224.4745	0.035 NM_199307	1.79	Ece1	endothelin converting enzyme 1	0001921 // positive regulation of receptor recycling // inferred from electronic annotation///004
66.02708 113.9495	0.027 NM_019763	1.78	Spn	SPEN homolog, transcriptional regulator (Drosophila)	0045892 // negative regulation of transcription, DNA-dependent // inferred from direct assay//
24.74597 44.40036	0.031 NM_010167	1.78	Eya4	eyes absent 4 homolog (Drosophila)	0007275 // multicellular organismal development // inferred from electronic annotation///0008
30.8225 53.1494	0.031 XM_001003576///XM	1.78	Rnf157	ring finger protein 157	0005515 // protein binding // inferred from electronic annotation///0046872 // metal ion bindir
198.9192 353.2621	0.013 NM_009288	1.77	Stk10	serine/threonine kinase 10	0006468 // protein amino acid phosphorylation // inferred from electronic annotation
107.5748 181.7082	0.048 XM_001478275///NN	1.77	Stk11ip1///LOC1000474	similar to serine/threonine kinase 11 interacting protein///serine/threonine kinase 11 interacting proteir	0003774 // motor activity // inferred from electronic annotation
76.59496 132.9639	0.022 NM_026599///XM_0i	1.77	Cgml1	cingulin-like 1	0016311 // dephosphorylation // inferred from electronic annotation///0006470 // protein amir
367.749 643.698	0.011 NM_011207	1.77	Ptpn3	protein tyrosine phosphatase, non-receptor type 3	0019941 // modification-dependent protein catabolic process // inferred from electronic annota
41.73602 72.87556	0.006 NM_025958	1.76	Cand2	cullin-associated and neddylation-dissociated 2 (putative)	0007264 // small GTPase mediated signal transduction // inferred from electronic annotation///
66.93405 113.8756	0.029 NM_001037136///NN	1.76	Agap1	ArfGAP with GTPase domain, ankyrin repeat and PH domain 1 (Agap1), tra	0019067 // viral assembly, maturation, egress, and release // inferred from electronic annotatio
220.5379 380.1808	0.016 NM_011046///NM_0	1.76	Furin	furin (paired basic amino acid cleaving enzyme)	0007185 // transmembrane receptor protein tyrosine phosphatase signaling pathway // inferrec
77.23624 132.5177	0.008 NM_011212	1.76	Ptpre	protein tyrosine phosphatase, receptor type, E	0016021 // integral to membrane // inferred from electronic annotation///0016020 // membrar
253.2188 435.5927	0.018 NM_172257	1.75	Sidt2	SID1 transmembrane family, member 2	0007520 // myoblast fusion // inferred from mutant phenotype///0030220 // platelet formation
909.9778 1564.273	0.009 NM_022410	1.75	Myh9	myosin, heavy polypeptide 9, non-muscle	0001558 // regulation of cell growth // inferred from electronic annotation
194.1107 333.0233	0.046 NM_015800	1.75	Crim1	cysteine rich transmembrane BMP regulator 1 (chordin like)	0030718 // germ-line stem cell maintenance // inferred from mutant phenotype///0006355 // r
175.302 299.1705	0.024 NM_001025432	1.75	Crebbp	CREB binding protein	0051402 // neuron apoptosis // inferred from direct assay///0006506 // GPI anchor biosynthetic
73.15476 127.3696	0.005 NM_133779	1.75	Pigt	phosphatidylinositol glycan anchor biosynthesis, class T	0007275 // multicellular organismal development // inferred from electronic annotation///0030
271.6172 465.2588	0.010 NM_010928	1.75	Notch2	Notch gene homolog 2 (Drosophila)	0019941 // modification-dependent protein catabolic process // inferred from electronic annota
194.5272 332.9098	0.010 XM_001479450///XM	1.74	Ubr4	ubiquitin protein ligase E3 component n-recognin 4	0005515 // protein binding // inferred from electronic annotation///0046872 // metal ion bindir
198.4744 332.1699	0.033 NM_153762	1.74	Rnf26	ring finger protein 26	0006270 // DNA replication initiation // inferred from electronic annotation///0006268 // DNA t
143.3857 239.6876	0.049 NM_008567	1.74	Mcm6	minichromosome maintenance deficient 6 (MISS homolog, S. pombe) (S. c	0030048 // actin filament-based movement // inferred from mutant phenotype///0006928 // ce
716.998 1223.807	0.023 NM_153423	1.74	Wasf2	WAS protein family, member 2	0007283 // spermatogenesis // inferred from mutant phenotype///0055114 // oxidation reducti
330.8602 563.0998	0.026 NM_015729	1.74	Acox1	Acyl-Coenzyme A oxidase 1, palmitoyl (Acox1), mRNA///acyl-Coenzyme A c	0007242 // intracellular signaling cascade // inferred from electronic annotation///0035023 // ri
83.03812 141.2276	0.031 NM_001081290	1.73	Bat2d	BAT2 domain containing 1	0005515 // protein binding // inferred from physical interaction
109.8652 183.4712	0.042 NM_001130152///NN	1.73	Arhgef1	Rho guanine nucleotide exchange factor (GEF) 1	0007049 // cell cycle // inferred from electronic annotation///0007165 // signal transduction //
8.889217 15.54586	0.021 NM_025413///NM_0	1.73	Lce1g///Lce1f///Lce1c	late cornified envelope 1G///late cornified envelope 1C///late cornified en	
68.44147 117.7525	0.002 NM_146258	1.73	Stard13	StAR-related lipid transfer (START) domain containing 13	

[ICR, PBS]([ICR, SUL])p	RefSeq Transcript ID	FC [PBS:SFN]	Gene Symbol	Gene Title	Gene Ontology Biological Process
2843.996 4773.549	0.035 NM_009255	1.73	Serpine2	serine (or cysteine) peptidase inhibitor, clade E, member 2	0007275 // multicellular organismal development // inferred from electronic annotation//0030
258.6336 437.6887	0.042 NM_001111121//XN	1.73	Ccdc6	coiled-coil domain containing 6	
275.6439 456.0472	0.048 NM_133791	1.73	Wwc2	WW, C2 and coiled-coil domain containing 2	0005515 // protein binding // inferred from electronic annotation
219.0385 366.4841	0.019 NM_010813	1.72	Mnt	max binding protein	0051726 // regulation of cell cycle // inferred from mutant phenotype//0006355 // regulation c
96.78254 165.8212	0.027 NM_008239	1.72	Foxq1	forkhead box Q1	0031069 // hair follicle morphogenesis // inferred from mutant phenotype//0006355 // regulat
16.96264 29.73057	0.039 NM_001081153	1.72	Unc13c	unc-13 homolog C (C. elegans)	0006887 // exocytosis // inferred from electronic annotation//0007242 // intracellular signaling
66.70499 111.6266	0.019 NM_009873	1.72	Cdk6	cyclin-dependent kinase 6	0007049 // cell cycle // inferred from electronic annotation//0043697 // cell dedifferentiation /
4320.835 7265.781	0.041 NM_001037859	1.72	Csf1r	colony stimulating factor 1 receptor	0007169 // transmembrane receptor protein tyrosine kinase signaling pathway // inferred from
65.67841 111.599	0.004 NM_011078	1.72	Phf2	PHD finger protein 2	0005515 // protein binding // inferred from electronic annotation//0046872 // metal ion bindir
167.588 282.5595	0.043 NM_177390	1.72	Myo1d	myosin ID	0003774 // motor activity // inferred from electronic annotation//0005524 // ATP binding // ini
230.6678 385.8307	0.013 NM_176850	1.72	Bptf	bromodomain PHD finger transcription factor	0006338 // chromatin remodeling // inferred from sequence or structural similarity//0045449 /
114.484 189.2923	0.038 NM_008224	1.71	Hcfc1	host cell factor C1	0007049 // cell cycle // inferred from electronic annotation//0019046 // reactivation of latent v
354.8626 586.1923	0.043 NM_009149	1.71	Glg1	golgi apparatus protein 1	0005529 // sugar binding // inferred from electronic annotation
154.8218 258.7969	0.014 NM_001159634//NN	1.71	Bat2l	HLA-B associated transcript 2-like	
450.1612 743.838	0.049 NM_015804	1.71	Atp11a	ATPase, class VI, type 11A	0015914 // phospholipid transport // inferred from electronic annotation//0006754 // ATP bios
73.63207 123.7675	0.021 NM_172856	1.71	Lass6	LAG1 homolog, ceramide synthase 6//LAG1 homolog, ceramide synthase	0030148 // sphingolipid biosynthetic process // inferred from direct assay//0046513 // ceramic
227.1453 384.099	0.017 NM_001013371	1.71	Dtx3l	deltex 3-like (Drosophila)	0005515 // protein binding // inferred from electronic annotation//0046872 // metal ion bindir
93.38088 158.1319	0.011 XM_893956//XM_9C	1.71	Mil5	myeloid/lymphoid or mixed-lineage leukemia 5	0016568 // chromatin modification // inferred from electronic annotation//0007049 // cell cycl
69.06372 114.7385	0.012 NM_013845	1.71	Ror1	receptor tyrosine kinase-like orphan receptor 1	0007169 // transmembrane receptor protein tyrosine kinase signaling pathway // inferred from
57.98469 97.48911	0.022 NM_033072	1.70	Mbd6	methyl-CpG binding domain protein 6	0003677 // DNA binding // inferred from electronic annotation
79.57723 132.5319	0.014 NM_001003912	1.70	Arhgef11	CDNA clone IMAGE:30669655//Rho guanine nucleotide exchange factor (0007242 // intracellular signaling cascade // inferred from electronic annotation//0035023 // r
425.1166 702.6921	0.029 NM_010638	1.70	Klf9	Kruppel-like factor 9	0007566 // embryo implantation // inferred from direct assay//0006355 // regulation of transc
82.32908 137.7479	0.035 NM_001081247	1.70	Polr3a	polymerase (RNA) III (DNA directed) polypeptide A	0006350 // transcription // inferred from electronic annotation
404.1304 662.8152	0.049 NM_001034030//NN	1.70	Limk2	LIM motif-containing protein kinase 2	0007283 // spermatogenesis // inferred from mutant phenotype//0006468 // protein amino ac
253.9015 425.1217	0.003 NM_178392	1.70	Snapc1	small nuclear RNA activating complex, polypeptide 1	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation//
199.7704 330.2058	0.021 XM_204015//NM_0I	1.69	Rere	arginine glutamic acid dipeptide (RE) repeats//Arginine glutamic acid dipe	0007275 // multicellular organismal development // inferred from electronic annotation//0006
117.0877 198.0725	0.011 NM_178242//XM_3I	1.69	Tnfr18	Zinc finger protein 469, mRNA (cDNA clone IMAGE:5321785)//triple	0006869 // lipid transport // inferred from electronic annotation
534.7604 880.5059	0.029 NM_138310	1.69	ApoB48r	apolipoprotein B48 receptor	0008202 // steroid metabolic process // inferred from electronic annotation//0006869 // lipid t
530.3486 889.2313	0.030 NM_001145970//NN	1.69	Mtap7d1	microtubule-associated protein 7 domain containing 1	0005819 // spindle // inferred from electronic annotation
508.8031 850.4089	0.007 XM_915167//XM_9I	1.69	Hectd1	HECT domain containing 1	0019941 // modification-dependent protein catabolic process // inferred from electronic annota
59.86271 97.55676	0.044 NM_134087	1.69	Fam83h	family with sequence similarity 83, member H	0001503 // ossification // inferred from electronic annotation
85.27836 141.1566	0.030 XM_907140//XM_1I	1.69	Akap13	A kinase (PRKA) anchor protein 13 (Akap13), mRNA//A kinase (PRKA) anch	0007242 // intracellular signaling cascade // inferred from electronic annotation//0035023 // r
72.97849 120.9264	0.011 NM_146129	1.69	Pcif1	PDX1 C-terminal inhibiting factor 1	0005515 // protein binding // inferred from electronic annotation
576.448 953.1678	0.008 NM_025994	1.69	Efh2	EF hand domain containing 2	0005509 // calcium ion binding // inferred from electronic annotation//0005515 // protein binc
420.6567 697.265	0.025 NM_009868	1.68	Cdh5	cadherin 5	0007156 // homophilic cell adhesion // inferred from electronic annotation//0007155 // cell ad
119.2826 197.0566	0.025 NM_178116	1.68	Camta2	calmodulin binding transcription activator 2	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation//
157.8581 257.3333	0.042 NM_030210	1.68	Aacs	acetoacetyl-CoA synthetase	0008152 // metabolic process // inferred from electronic annotation//0006629 // lipid metabol
84.953 139.014	0.022 NM_153062	1.68	Slc37a1	solute carrier family 37 (glycerol-3-phosphate transporter), member 1	
564.3482 923.8051	0.026 NM_030249	1.68	Cttnbp2nl	CTTNBP2 N-terminal like	0005730 // nucleolus // inferred from electronic annotation//0015629 // actin cytoskeleton // i
340.7094 553.8533	0.043 NM_009282//XM_0I	1.68	LOC100045442//Stag	similar to Stromal antigen 1//stromal antigen 1	0051301 // cell division // inferred from electronic annotation//0007049 // cell cycle // inferrec
64.18406 103.9823	0.045 NM_001080931	1.68	Med13	mediator complex subunit 13	0006357 // regulation of transcription from RNA polymerase II promoter // inferred from electr
870.7371 1435.444	0.049 NM_028072	1.68	Sulf2	sulfatase 2	0008152 // metabolic process // inferred from electronic annotation//0006790 // sulfur metab
287.9308 467.1397	0.041 NM_009282//XM_0I	1.67	LOC100045442//Stag	similar to Stromal antigen 1//Stromal antigen 1 (Stag1), mRNA//stromal	0051301 // cell division // inferred from electronic annotation//0007049 // cell cycle // inferrec
166.9485 274.9643	0.005 NM_018748	1.67	Golga4	golgi autoantigen, golgin subfamily a, 4	0005794 // Golgi apparatus // inferred from direct assay//0000139 // Golgi membrane // inferr
1454.582 2394.269	0.025 NM_145928	1.67	Tspan14	tetraspanin 14	0016021 // integral to membrane // inferred from electronic annotation//0016020 // membrar
205.019 332.0504	0.046 NM_001033198	1.67	Ankrd50	ankyrin repeat domain 50	
268.3549 432.1902	0.040 NM_007516//NM_0	1.67	Hnrnpd	heterogeneous nuclear ribonucleoprotein D	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation//
653.0924 1060.732	0.022 NM_010123	1.67	Eif3a	eukaryotic translation initiation factor 3, subunit A	0001732 // formation of translation initiation complex // inferred from direct assay//0006412 /
196.5726 138.9371	0.038 NM_011417	1.67	Smarca4	SWI/SNF related, matrix associated, actin dependent regulator of chromati	0006334 // nucleosome assembly // traceable author statement//0030198 // extracellular mat
3339.432 5442.125	0.021 NM_026381//NM_0	1.67	Shisa5	shisa homolog 5 (Xenopus laevis)	0006915 // apoptosis // inferred from electronic annotation//0006915 // apoptosis // inferred
914.905 1483.796	0.018 NM_010301	1.67	Gna11	guanine nucleotide binding protein, alpha 11	0007186 // G-protein coupled receptor protein signaling pathway // inferred from mutant phen
32.27441 53.55214	0.015 NM_133957//NM_0	1.67	Nfat5	Nuclear factor of activated T-cells 5 (Nfat5), transcript variant a, mRNA//n	0001816 // cytokine production // inferred from direct assay//0006355 // regulation of transcr
85.27412 137.1208	0.038 NM_172689	1.66	Ddx58	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	0009615 // response to virus // inferred from electronic annotation//0045087 // innate immun
587.9249 950.9334	0.041 NM_133758	1.66	Usp47	ubiquitin specific peptidase 47	0019941 // modification-dependent protein catabolic process // inferred from electronic annota
359.9723 594.2253	0.026 NM_146099	1.66	D19Wsu162e	DNA segment, Chr 19, Wayne State University 162, expressed	0016021 // integral to membrane // inferred from electronic annotation//0016020 // membrar
6210.787 9975.187	0.045 NM_011576	1.66	Tfpi	tissue factor pathway inhibitor	0007596 // blood coagulation // inferred from electronic annotation
241.8179 390.9808	0.019 NM_133665	1.66	Mef2d	myocyte enhancer factor 2D	0006915 // apoptosis // inferred from electronic annotation//0007275 // multicellular organisn
154.3802 252.1895	0.014 NM_007865	1.66	Dll1	delta-like 1 (Drosophila)	0007275 // multicellular organismal development // inferred from electronic annotation//0009
16.28592 27.11514	0.017 NM_178655//NM_0	1.66	Ank2	ankyrin 2, brain	0007165 // signal transduction // inferred from electronic annotation//0034394 // protein loca
176.6948 286.5571	0.033 NM_144868	1.65	Pcnx13	pecanex-like 3 (Drosophila)	0016021 // integral to membrane // inferred from electronic annotation//0016020 // membrar

[ICR, PBS]([ICR, SUL])p	RefSeq Transcript ID	FC [PBS:SFN]	Gene Symbol	Gene Title	Gene Ontology Biological Process
224.0976 357.7112	0.041 NM_001001144///NM	1.65	<i>Scap</i>	SREBF chaperone	0008202 // steroid metabolic process // inferred from electronic annotation///0008203 // chole
254.8455 413.8673	0.006 NM_013651	1.65	<i>Sf3a2</i>	splicing factor 3a, subunit 2	0008380 // RNA splicing // inferred from electronic annotation///0006397 // mRNA processing /
82.91287 133.9181	0.006 NM_001081373	1.64	<i>Cep164</i>	centrosomal protein 164	0006974 // response to DNA damage stimulus // inferred from electronic annotation///0051301
307.0527 492.6299	0.020 NM_148932	1.64	<i>Pom121</i>	nuclear pore membrane protein 121	0051028 // mRNA transport // inferred from electronic annotation///0065002 // intracellular pr
29.4817 49.10988	0.048 NR_001461	1.64	<i>Kcnq1ot1</i>	KCNQ1 overlapping transcript 1	0016458 // gene silencing // inferred from direct assay///0010216 // maintenance of DNA meth
121.2904 199.9306	0.030 NM_175666	1.63	<i>Hist2h2bb</i>	histone locus 2, H2bb	0006334 // nucleosome assembly // inferred from electronic annotation
130.1009 209.0963	0.010 NM_009089	1.63	<i>Polr2a</i>	polymrase (RNA) II (DNA directed) polypeptide A	0006366 // transcription from RNA polymerase II promoter // inferred from electronic annotati
92.93684 149.5848	0.008 XR_032210	1.63	<i>LOC100045684</i>	similar to N-myristoyltransferase 1	
454.8436 739.0208	0.016 NM_010253	1.63	<i>Gal</i>	galanin	0006950 // response to stress // inferred from electronic annotation///0031943 // regulation of
198.0269 318.2334	0.011 NM_010111	1.63	<i>Efnb2</i>	ephrin B2	0007275 // multicellular organismal development // inferred from electronic annotation///0001
49.54213 80.23303	0.038 NM_026083	1.63	<i>Zc3h13</i>	zinc finger CCHC type containing 13	0046872 // metal ion binding // inferred from electronic annotation///0008270 // zinc ion bindi
539.9053 881.6233	0.038 NM_011058///NM_0	1.63	<i>Pdgfra</i>	platelet derived growth factor receptor, alpha polypeptide	0060021 // palate development // inferred from mutant phenotype///0060325 // face morphog
96.56848 156.9758	0.024 NM_170599	1.62	<i>Igfb1</i>	immunoglobulin superfamily, member 11	0007155 // cell adhesion // inferred from electronic annotation///0040008 // regulation of grow
306.019 480.1687	0.038 NM_138659	1.62	<i>Prpf8</i>	pre-mRNA processing factor 8	0008380 // RNA splicing // inferred from electronic annotation///0006397 // mRNA processing /
66.96044 109.5213	0.043 NM_001033212	1.62	<i>Rprml</i>	reprimin-like	0016021 // integral to membrane // inferred from electronic annotation///0016020 // membrar
128.9385 203.384	0.028 NM_057171	1.62	<i>Bat3</i>	HLA-B-associated transcript 3	0042981 // regulation of apoptosis // inferred from reviewed computational analysis///0006915
63.85999 100.1216	0.028 NM_011379	1.61	<i>Sipa1</i>	signal-induced proliferation associated gene 1	0051726 // regulation of cell cycle // inferred from direct assay///0051056 // regulation of small
180.3007 287.9438	0.023 NM_023544///NM_0	1.61	<i>Rsc1a1///Ddi2</i>	DNA-damage inducible protein 2///regulatory solute carrier protein, family	0051051 // negative regulation of transport // inferred from electronic annotation///0050892 //
550.3471 888.0051	0.034 NM_011480	1.61	<i>Sreb1</i>	sterol regulatory element binding transcription factor 1	0008202 // steroid metabolic process // inferred from electronic annotation///0006355 // regul.
199.9897 312.6738	0.031 NM_022882	1.61	<i>Lpin2</i>	Lipin 2, mRNA (cDNA clone MGC:46819 IMAGE:5101211)///lipin 2	0008195 // phosphatidate phosphatase activity // inferred from direct assay
144.9849 229.1207	0.015 NM_028412	1.61	<i>Ciz1</i>	CDKN1A interacting zinc finger protein 1	0046872 // metal ion binding // inferred from electronic annotation///0008270 // zinc ion bindi
36.40942 57.92859	0.002 NM_009297	1.61	<i>Supt6h</i>	suppressor of Ty 6 homolog (S. cerevisiae)	0006357 // regulation of transcription from RNA polymerase II promoter // inferred from electr
57.29696 91.00245	0.024 NM_001033759///NM	1.61	<i>Tmem2</i>	Transmembrane protein 2 (Tmem2), transcript variant 1, mRNA///transme	0016021 // integral to membrane // inferred from electronic annotation///0016020 // membrar
23.34509 37.35414	0.005 NM_009405	1.61	<i>Tnni2</i>	troponin I, skeletal, fast 2	0045941 // positive regulation of transcription // inferred from electronic annotation///0003005
92.19415 146.5433	0.001 NM_001114386///NM	1.61	<i>Nedd4l</i>	neural precursor cell expressed, developmentally down-regulated gene 4-l	0010766 // negative regulation of sodium ion transport // inferred from direct assay///0019941
377.2236 592.6205	0.021 NM_001005331///NM	1.61	<i>Elf4g1</i>	eukaryotic translation initiation factor 4, gamma 1	0006412 // translation // inferred from electronic annotation///0016070 // RNA metabolic proci
88.74268 138.6623	0.042 NM_022022///XM_0	1.61	<i>Ube4b</i>	ubiquitination factor E4B, UFD2 homolog (S. cerevisiae)///Ubiquitination f	0019941 // modification-dependent protein catabolic process // inferred from electronic annota
160.3729 252.7411	0.004 NM_153103	1.60	<i>Kif1c</i>	kinesin family member 1C	0006890 // retrograde vesicle-mediated transport, Golgi to ER // inferred from direct assay///00
197.9069 313.0269	0.005 NM_021899	1.60	<i>Foxj2</i>	forkhead box J2	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation//
189.385 307.7082	0.046 NM_024440	1.60	<i>Derl3</i>	Der1-like domain family, member 3	0005783 // endoplasmic reticulum // inferred from electronic annotation///0005789 // endopla
414.1126 655.2076	0.021 NM_009593	1.60	<i>Abcg1</i>	ATP-binding cassette, sub-family G (WHITE), member 1	0006869 // lipid transport // inferred from electronic annotation///0045449 // regulation of trar
60.70678 95.99432	0.005 NM_144812///NM_1	1.60	<i>Tnrc6b</i>	trinucleotide repeat containing 6b	0006417 // regulation of translation // inferred from electronic annotation///0031047 // gene si
599.9963 956.6914	0.031 NM_011498	1.60	<i>Bhlhe40</i>	basic helix-loop-helix family, member e40	0045892 // negative regulation of transcription, DNA-dependent // inferred from direct assay//
175.181 271.003	0.043 NM_008633	1.60	<i>Mtap4</i>	microtubule-associated protein 4	0007026 // negative regulation of microtubule depolymerization // inferred from electronic ann
1377.441 2192.68	0.027 NM_173182	1.60	<i>Fndc3b</i>	fibronectin type III domain containing 3B	0045600 // positive regulation of fat cell differentiation // inferred from physical interaction
186.8104 290.671	0.044 NM_027144	1.60	<i>Arhgef12</i>	Rho guanine nucleotide exchange factor (GEF) 12	0007242 // intracellular signaling cascade // inferred from electronic annotation///0007186 // G
1313.981 2044.088	0.029 NM_146130///XM_8	1.59	<i>LOC100045099///OTTI</i>	predicted gene, EG627828///predicted gene, OTTMUSG00000004599///si	0008380 // RNA splicing // inferred from electronic annotation///0006397 // mRNA processing /
99.51416 153.988	0.049 NM_001081255	1.59	<i>Lrch3</i>	Leucine-rich repeats and calponin homology (CH) domain containing 3, mR	0005515 // protein binding // inferred from electronic annotation
99.03201 157.2356	0.015 NM_021521	1.59	<i>Med12</i>	mediator of RNA polymerase II transcription, subunit 12 homolog (yeast)	0035176 // social behavior // inferred from mutant phenotype///0006357 // regulation of transi
116.5475 181.5619	0.031 NM_138679	1.59	<i>Ash1</i>	ash1 (absent, small, or homeotic)-like (Drosophila)	0016568 // chromatin modification // inferred from electronic annotation///0006355 // regulati
305.6621 481.4534	0.002 NM_001145952///NM	1.59	<i>Lpp</i>	LIM domain containing preferred translocation partner in lipoma///LIM do	0007155 // cell adhesion // inferred from electronic annotation
89.41513 141.7813	0.029 XM_001481284///XN	1.59	<i>Wipf3</i>	WAS/WASL interacting protein family, member 3	0007275 // multicellular organismal development // inferred from electronic annotation///0030
472.7928 762.8283	0.048 NM_172685	1.59	<i>Slc25a24</i>	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member	0006810 // transport // inferred from electronic annotation
148.7044 229.8842	0.043 XM_001476519///NM	1.59	<i>Brd1///LOC100045983</i>	similar to bromodomain containing 1///bromodomain containing 1	0005515 // protein binding // inferred from electronic annotation///0046872 // metal ion bindir
61.34346 98.28765	0.032 NM_008616///NM_0	1.59	<i>Zfp239</i>	zinc finger protein 239	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation//
481.8109 748.8629	0.031 NM_009045	1.59	<i>Rela</i>	v-rel reticuloendotheliosis viral oncogene homolog A (avian)	0051092 // positive regulation of NF-kappaB transcription factor activity // inferred from electro
394.1875 616.3745	0.016 NM_175344	1.58	<i>Ano6</i>	anoctamin 6	0006811 // ion transport // inferred from electronic annotation///0006810 // transport // inferr
143.186 221.0468	0.026 NM_010613	1.58	<i>Khsrp</i>	KH-type splicing regulatory protein	0006412 // translation // inferred from electronic annotation///0051028 // mRNA transport // i
92.5527 144.7332	0.024 NM_001081057	1.58	<i>Tecpr2</i>	tectonin beta-propeller repeat containing 2	0005634 // nucleus // inferred from electronic annotation///0005737 // cytoplasm // inferred fr
340.354 533.0895	0.021 NM_001033275	1.58	<i>Glt8d3</i>	glycosyltransferase 8 domain containing 3	0016757 // transferase activity, transferring glycosyl groups // inferred from electronic annotati
334.4582 514.9414	0.033 NM_007460	1.58	<i>Ap3d1</i>	adaptor-related protein complex 3, delta 1 subunit	0048007 // antigen processing and presentation, exogenous lipid antigen via MHC class Ib // infe
119.3363 183.6027	0.038 NM_145970	1.58	<i>Cc2d1a</i>	coiled-coil and C2 domain containing 1A	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation//
261.5124 401.6401	0.032 NM_133947	1.58	<i>Numa1</i>	Nuclear mitotic apparatus protein 1 (Numa1), mRNA///nuclear mitotic app	0051321 // meiotic cell cycle // inferred from electronic annotation
557.5716 859.9428	0.036 NM_146012///XR_03	1.58	<i>Ctdsp2///ENSMUSG00</i>	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small ph	0016791 // phosphatase activity // inferred from electronic annotation///0004721 // phosphop
59.91959 92.56378	0.015 NM_001114609///NM	1.58	<i>Ino80d</i>	INO80 complex subunit D	
178.9488 274.9617	0.027 NM_007795	1.58	<i>Ctf1</i>	cardiotrophin 1	0048666 // neuron development // inferred from genetic interaction
40.61821 63.71928	0.006 XM_001477657///XN	1.58	<i>BC059842</i>	cDNA sequence BC059842///PREDICTED: Mus musculus cDNA sequence BC059842 (BC059842), mRNA	
272.0418 421.186	0.031 NM_001081298///XR	1.58	<i>Lphn2///LOC10004805</i>	latrophilin 2///similar to calcium-independent alpha-latrotoxin receptor hc	0007165 // signal transduction // inferred from electronic annotation///0007218 // neuropeptid
48.78642 75.21652	0.049 NM_017401	1.58	<i>Polm</i>	polymerase (DNA directed), mu	0030183 // B cell differentiation // inferred from mutant phenotype///0016446 // somatic hype
112.555 176.6525	0.026 NM_009755	1.57	<i>Bmp1</i>	bone morphogenetic protein 1	0001503 // ossification // inferred from electronic annotation///0007275 // multicellular organi

[ICR, PBS]([ICR, SUL])p	RefSeq Transcript ID	FC [PBS:SFN]	Gene Symbol	Gene Title	Gene Ontology Biological Process
429.6642 662.8736	0.010 NM_133852///NM_0	1.57	Golga2	golgi autoantigen, golgin subfamily a, 2	0005515 // protein binding // inferred from electronic annotation
81.00088 124.2209	0.031 NM_181071	1.57	Tanc2	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2	0005488 // binding // inferred from electronic annotation
127.7242 198.16	0.000 NM_007772	1.57	Hivp1	human immunodeficiency virus type I enhancer binding protein 1	0045892 // negative regulation of transcription, DNA-dependent // inferred from direct assay//
56.00654 86.90212	0.024 NM_177136///NM_0	1.57	Fryl	furry homolog-like (Drosophila)	0005488 // binding // inferred from electronic annotation//0005515 // protein binding // infer
101.7255 155.3127	0.047 NM_001029994///NM	1.57	Zc3h18	zinc finger CCHC-type containing 18	0046872 // metal ion binding // inferred from electronic annotation//0008270 // zinc ion bindi
138.0526 214.6047	0.011 NM_001017427	1.57	Rasef	RAS and EF hand domain containing	0007264 // small GTPase mediated signal transduction // inferred from electronic annotation//
140.3343 216.3232	0.022 NM_001003815///NM	1.57	Epb4.11	erythrocyte protein band 4.1-like 1	0030866 // cortical actin cytoskeleton organization // inferred from electronic annotation
89.84402 139.3159	0.050 NM_001039530	1.57	Parp14	poly (ADP-ribose) polymerase family, member 14	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation//
116.495 179.0293	0.015 NM_177592	1.56	Tmem164	transmembrane protein 164///CDNA clone IMAGE:6815971	0016021 // integral to membrane // inferred from electronic annotation//0016020 // membr
632.6245 970.8284	0.033 NM_145629	1.56	Pls3	plastin 3 (T-isoform)	0007015 // actin filament organization // inferred from electronic annotation
74.1358 113.022	0.025 NM_009744	1.56	Bcl6	B-cell leukemia/lymphoma 6	0043380 // regulation of memory T cell differentiation // inferred from mutant phenotype//000
18.41829 28.43762	0.041 NM_199222	1.56	Lman1l	lectin, mannose-binding 1 like	0005529 // sugar binding // inferred from electronic annotation
713.3142 1101.267	0.026 NM_207515///NM_1	1.56	Mbnl2	muscleblind-like 2///MKIAA4072 protein	0003723 // RNA binding // inferred from electronic annotation//0046872 // metal ion binding /
350.8924 536.263	0.029 NM_054097	1.56	Pip4k2c	phosphatidylinositol-5-phosphate 4-kinase, type II, gamma	0046488 // phosphatidylinositol metabolic process // inferred from electronic annotation
170.4751 262.1913	0.007 NM_009848	1.56	Entpd1	ectonucleoside triphosphate diphosphohydrolase 1	0030168 // platelet activation // inferred from direct assay//0009181 // purine ribonucleoside
29.36248 44.99492	0.010 NM_011518	1.56	Syk	Spleen tyrosine kinase (Syk), mRNA///spleen tyrosine kinase	0050731 // positive regulation of peptidyl-tyrosine phosphorylation // inferred from mutant phe
455.575 697.1745	0.008 NM_181594	1.56	Edc4	enhancer of mRNA decapping 4	0005515 // protein binding // inferred from electronic annotation
151.4481 229.5615	0.033 NM_033144	1.55	8-Sep	septin 8	0007049 // cell cycle // inferred from electronic annotation
194.0777 294.0106	0.042 XM_001474137///NM	1.55	LOC100043998///Tpr	translocated promoter region///similar to nuclear pore complex-associated	0006412 // translation // inferred from electronic annotation//0006434 // seryl-tRNA aminoacyl
101.6337 157.5316	0.038 NM_183017	1.55	Ttl12	TTL domain protein (Ttl12 gene), strain C57BL6///tubulin tyrosine ligase-III	0006464 // protein modification process // inferred from electronic annotation
29.29646 44.46393	0.031 NM_133667	1.55	Pdk2	pyruvate dehydrogenase kinase, isoenzyme 2	0007165 // signal transduction // inferred from electronic annotation//0005975 // carbohydrat
219.2237 334.5379	0.019 NM_130863	1.55	Adrbk1	adrenergic receptor kinase, beta 1	0016310 // phosphorylation // inferred from electronic annotation//0007165 // signal transduc
1136.67 1717.159	0.043 NM_001033268	1.55	Fam120a	family with sequence similarity 120, member A	0003723 // RNA binding // inferred from electronic annotation
68.28994 103.982	0.011 NM_001044719///NM	1.55	D17Wsu92e	DNA segment, Chr 17, Wayne State University 92, expressed///DNA segment, Chr 17, Wayne State University 92, expressed, mRNA (cDNA clone MGC:178969 IMAGE:9053)	0006544 // glycine metabolic process // inferred from electronic annotation//0006563 // L-seri
79.57266 122.4096	0.014 NM_028230	1.55	Shmt2	serine hydroxymethyltransferase 2 (mitochondrial)	0006468 // protein amino acid phosphorylation // inferred from electronic annotation
233.1955 357.2964	0.014 NM_007908	1.55	Eef2k	eukaryotic elongation factor-2 kinase	0019941 // modification-dependent protein catabolic process // inferred from electronic annota
310.8276 479.9587	0.045 NM_007707	1.55	Socs3	suppressor of cytokine signaling 3	
50.73664 76.76267	0.037 NM_001001738	1.55	Itrip	inositol 1,4,5-triphosphate receptor interacting protein	
211.457 322.2477	0.005 NM_153533	1.55	Tenc1	tensin like C1 domain-containing phosphatase	0048871 // multicellular organismal homeostasis // inferred from mutant phenotype//0001822
97.72817 148.2722	0.034 NM_144872	1.55	Eml3	echinoderm microtubule associated protein like 3	0005874 // microtubule // inferred from electronic annotation//0005737 // cytoplasm // infer
46.74178 71.18797	0.049 NM_153543	1.55	Aldh12	aldehyde dehydrogenase 1 family, member L2	0055114 // oxidation reduction // inferred from electronic annotation//0009058 // biosyntheti
66.26363 100.0645	0.019 NM_001110132///NM	1.55	Cic	capicua homolog (Drosophila)	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation//
104.5636 156.971	0.033 NM_173048	1.54	Gga3	golgi associated, gamma adaptin ear containing, ARF binding protein 3	0006810 // transport // inferred from electronic annotation//0016192 // vesicle-mediated tran
105.2669 161.4533	0.011 NM_011424	1.54	Ncor2	nuclear receptor co-repressor 2	0045892 // negative regulation of transcription, DNA-dependent // inferred from direct assay//
665.6628 1000.735	0.043 NM_144530	1.54	Zc3h11a	zinc finger CCHC type containing 11A	0046872 // metal ion binding // inferred from electronic annotation//0008270 // zinc ion bindi
199.9942 301.5945	0.022 NM_015731	1.54	Atp9a	ATPase, class II, type 9A	0008152 // metabolic process // inferred from electronic annotation//0015914 // phospholipid
139.263 207.8604	0.034 NM_023544///NM_0	1.53	Rsc1a1///Ddi2	DNA-damage inducible protein 2///regulatory solute carrier protein, family	0051051 // negative regulation of transport // inferred from electronic annotation//0050892 //
910.7809 1369.686	0.015 NM_146130///XM_8	1.53	LOC100045099///OTT	predicted gene, EG627828///predicted gene, OTTMUSG00000004599///si	0008380 // RNA splicing // inferred from electronic annotation//0006397 // mRNA processing /
24.45775 36.78954	0.029 NM_027560	1.53	Arddc2	arrestin domain containing 2	
239.7012 362.9312	0.005 NM_011682	1.53	Utrn	utrophin	0007528 // neuromuscular junction development // inferred from electronic annotation//0007
317.4151 474.4151	0.042 NM_133221	1.53	Slc24a6	solute carrier family 24 (sodium/potassium/calcium exchanger), member 6	0006816 // calcium ion transport // inferred from electronic annotation//0006814 // sodium io
244.6859 370.7276	0.028 NM_019651	1.53	Ptpn9	protein tyrosine phosphatase, non-receptor type 9	0016311 // dephosphorylation // inferred from electronic annotation//0006470 // protein amir
78.12888 116.8522	0.029 NM_178236///NR_0C	1.53	Asb7	ankyrin repeat and SOCS box-containing 7	0019941 // modification-dependent protein catabolic process // inferred from electronic annota
34.23529 51.80119	0.045 NM_010820	1.53	Mpdz	multiple PDZ domain protein	0007155 // cell adhesion // inferred from direct assay
59.79078 89.56892	0.046 NM_025690///NM_0	1.53	Sltn	SAFB-like, transcription modulator	0006915 // apoptosis // inferred from electronic annotation//0006355 // regulation of transcrip
59.55757 88.93058	0.033 NM_145416	1.52	Kri1	KRI1 homolog (S. cerevisiae)	
21.31657 32.06295	0.027 NM_009004	1.52	Kif20a	kinesin family member 20A	0006810 // transport // inferred from electronic annotation//0007018 // microtubule-based m
116.8092 174.9726	0.014 NM_194346	1.52	Rnf31	ring finger protein 31	0016874 // ligase activity // inferred from electronic annotation//0046872 // metal ion binding
168.064 251.2349	0.020 NM_133940	1.52	Fbxl14	F-box and leucine-rich repeat protein 14	0019941 // modification-dependent protein catabolic process // inferred from electronic annota
62.99466 93.62002	0.036 NM_033523	1.52	Spred2	spontin-related, EVH1 domain containing 2	0007275 // multicellular organismal development // inferred from electronic annotation//0000
133.6452 199.1525	0.018 NM_021280	1.52	Plcg1	Phospholipase C, gamma 1 (Plcg1), mRNA///phospholipase C, gamma 1	0050852 // T cell receptor signaling pathway // inferred from direct assay//0016042 // lipid cat
310.7354 463.7519	0.015 XR_035649///NM_00	1.52	EG666167///Ewsr1	predicted gene, EG666167///Ewing sarcoma breakpoint region 1	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation//
49.95923 73.98124	0.045 XR_034155///NM_00	1.51	LOC100048010///Cbl	Casitas B-lineage lymphoma///Casitas B-lineage lymphoma (Cbl), mRNA///	0019941 // modification-dependent protein catabolic process // inferred from electronic annota
188.6133 277.9381	0.024 NM_033371	1.51	Ppp1r16a	protein phosphatase 1, regulatory (inhibitor) subunit 16A	0005829 // cytosol // traceable author statement//0016020 // membrane // inferred from elec
140.9047 206.8401	0.031 NM_033563	1.51	Klf7	Kruppel-like factor 7 (ubiquitous)	0048813 // dendrite morphogenesis // inferred from mutant phenotype//0007409 // axonog
171.6281 253.4763	0.021 NM_001081685///NM	1.51	Zfp295	zinc finger protein 295	0005622 // intracellular // inferred from electronic annotation
120.1808 178.7498	0.039 NM_001081132	1.50	Upf2	UPF2 regulator of nonsense transcripts homolog (yeast)	0006986 // response to unfolded protein // not recorded//0016070 // RNA metabolic process /
70.50968 103.7012	0.029 NM_174868	1.50	Fam73a	family with sequence similarity 73, member A	0016021 // integral to membrane // inferred from electronic annotation//0016020 // membr
120.1555 177.9817	0.026 NM_199028	1.50	Bend3	BEN domain containing 3	
466.7545 695.7762	0.009 NM_030238	1.50	Dync1h1	dynein cytoplasmic 1 heavy chain 1	0007018 // microtubule-based movement // inferred from electronic annotation

[ICR, PBS]([ICR, SUL])p	RefSeq Transcript ID	FC [PBS:SFN]	Gene Symbol	Gene Title	Gene Ontology Biological Process
206.2862 307.6928	0.011 NM_026014		1.50 Cdt1	chromatin licensing and DNA replication factor 1	0000076 // DNA replication checkpoint // inferred from electronic annotation///0000076 // DN
152.0945 226.2159	0.012 NM_001114097///NM		1.50 Smarcc2	SWI/SNF related, matrix associated, actin dependent regulator of chromati	0016568 // chromatin modification // inferred from electronic annotation///0006355 // regulati
222.6589 145.6392	0.010 NM_025683		-1.50 Rpe	ribulose-5-phosphate-3-epimerase	0008152 // metabolic process // inferred from electronic annotation///0005975 // carbohydrate
656.3445 432.1881	0.004 NM_001130149///NM		-1.50 LOC100045148///Rnas	ribonuclease III, nuclear///similar to ribonuclease III, nuclear	0006396 // RNA processing // inferred from electronic annotation
663.184 435.0452	0.025 NM_145392		-1.51 Bag2	BCL2-associated athanogene 2	0019538 // protein metabolic process // inferred from electronic annotation///0006915 // apop
980.876 638.2849	0.011 NM_145405		-1.51 Ubl4	ubiquitin-like 4	0006464 // protein modification process // inferred from electronic annotation
154.1863 100.299	0.032 NM_145133		-1.51 Tifa	TRAF-interacting protein with forkhead-associated domain	0007249 // I-kappaB kinase/NF-kappaB cascade // inferred from direct assay
510.9264 331.0704	0.023 NM_011883///NM_0		-1.51 Rnf13	ring finger protein 13	0005515 // protein binding // inferred from electronic annotation///0046872 // metal ion bindir
416.1779 267.4393	0.049 NM_029581		-1.51 Mti3	mitochondrial translational initiation factor 3	0032790 // ribosome disassembly // inferred from sequence or structural similarity///0006446 /
1091.826 710.4048	0.047 XM_001474604///NM		-1.51 Higd1a///LOC1000457	predicted gene, ENSMUSG00000044330///HIG1 domain family, member 1	0006950 // response to stress // inferred from electronic annotation
1168.432 769.4538	0.045 NM_026878		-1.52 Rasl11b	RAS-like, family 11, member B	0007264 // small GTPase mediated signal transduction // inferred from electronic annotation
1380.347 893.762	0.011 NM_025848		-1.52 Sdhb	succinate dehydrogenase complex, subunit D, integral membrane protein	0006810 // transport // inferred from electronic annotation///0006099 // tricarboxylic acid cycl
518.5929 332.9025	0.018 NM_026276		-1.52 Aasdhppt	aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transfe	0009059 // macromolecule biosynthetic process // inferred from electronic annotation
131.5069 84.73762	0.013 NM_025408		-1.52 Acer3	alkaline ceramidase 3	0006672 // ceramide metabolic process // inferred from electronic annotation
1884.869 1213.266	0.034 XM_001478170///NM		-1.52 Nae1///LOC10004739	similar to Amyloid beta precursor protein binding protein 1///NEDD8 activ	0019941 // modification-dependent protein catabolic process // inferred from electronic annota
172.7651 111.0249	0.012 NM_194269		-1.52 Morn2	MORN repeat containing 2	
1949.802 1261.678	0.017 NM_016778		-1.52 Bok	BCL2-related ovarian killer protein	0006915 // apoptosis // inferred from electronic annotation///0006917 // induction of apoptosi
2497.827 1613.335	0.017 NM_029478		-1.52 Tmem49	transmembrane protein 49	0005783 // endoplasmic reticulum // inferred from electronic annotation///0033116 // ER-Golgi
83.85282 54.2442	0.020 NM_010839///NM_0		-1.52 Mtcp1	mature T-cell proliferation 1	0005739 // mitochondrion // inferred from electronic annotation///0005739 // mitochondrion /
642.4833 411.8186	0.020 NM_026794		-1.52 Deb1	differentially expressed in B16F10 1	
953.4912 615.7377	0.007 NM_011851		-1.52 Nt5e	5' nucleotidase, ecto///5' nucleotidase, ecto (Nt5e), mRNA	0050728 // negative regulation of inflammatory response // inferred from mutant phenotype///
425.273 274.5216	0.021 NM_026959		-1.52 Stx18	synaptaxin 18	0006810 // transport // inferred from electronic annotation///0016192 // vesicle-mediated tran
290.2039 187.0178	0.010 NM_175560///NM_1		-1.53 9130019022Rik///Zfp	zinc finger protein 747///RIKEN cDNA 9130019022 gene///RIKEN cDNA E4	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation//
41.79565 26.98269	0.002 NM_026734		-1.53 Tmem126b	transmembrane protein 126B	0016021 // integral to membrane // inferred from electronic annotation///0016020 // membrar
106.1479 68.0648	0.030 NM_001077713		-1.53 Acn9	ACN9 homolog (S. cerevisiae)	0006094 // gluconeogenesis // inferred from sequence or structural similarity
3946.493 2540.61	0.029 NM_013470		-1.53 Anxa3	annexin A3	0019834 // phospholipase A2 inhibitor activity // inferred from electronic annotation///000554
33.78617 21.66928	0.045 NM_053253		-1.53 Zmynd10	zinc finger, MYND domain containing 10	0046872 // metal ion binding // inferred from electronic annotation///0008270 // zinc ion bindi
1462.523 947.2139	0.012 NM_144897		-1.53 Apoa1bp	apolipoprotein A-1 binding protein	0005515 // protein binding // not recorded
315.7233 202.5707	0.009 NM_172988		-1.53 Fbxl4	F-box and leucine-rich repeat protein 4	0019941 // modification-dependent protein catabolic process // inferred from electronic annota
489.8318 317.1462	0.033 NM_001081233///XR		-1.53 EG433923///Slc25a5//	predicted gene, EG433923///predicted gene, EG667030///predicted gene,	0006810 // transport // inferred from electronic annotation
2932.246 1880.48	0.048 XM_001474604///NM		-1.53 Higd1a///LOC1000457	predicted gene, ENSMUSG00000044330///HIG1 domain family, member 1	0006950 // response to stress // inferred from electronic annotation
921.4403 585.7483	0.020 NM_007530		-1.53 Bcap29	B-cell receptor-associated protein 29	0006915 // apoptosis // inferred from electronic annotation///0006810 // transport // inferred f
535.4031 342.8602	0.037 NM_024174		-1.54 Mrps23	mitochondrial ribosomal protein S23	0003735 // structural constituent of ribosome // inferred from sequence or structural similarity
464.3846 303.42	0.040 NM_175116		-1.54 P2ry5	purinergic receptor P2Y, G-protein coupled, 5	0007165 // signal transduction // inferred from electronic annotation///0007186 // G-protein cc
500.6631 318.0464	0.021 NM_001082532		-1.54 Pigyl	phosphatidylinositol glycan anchor biosynthesis, class Y-like	0006506 // GPI anchor biosynthetic process // inferred from electronic annotation
13.11494 8.277576	0.030 XM_001480867///XM		-1.54 Cd27	CD27 antigen	0048305 // immunoglobulin secretion // non-traceable author statement///0006915 // apoptos
988.4976 628.9379	0.047 NM_144916		-1.54 Tmem150	transmembrane protein 150	0016021 // integral to membrane // inferred from electronic annotation///0016021 // integral t
596.5231 377.851	0.028 NM_025301		-1.55 Mrpl17	mitochondrial ribosomal protein L17	0006412 // translation // not recorded///0006412 // translation // inferred from electronic ann
476.4685 299.4194	0.026 NM_023203		-1.55 Dctpp1	dCTP pyrophosphatase 1	0051289 // protein homotetramerization // inferred from direct assay
91.72947 58.15486	0.013 NM_025469		-1.55 Clps	colipase, pancreatic	0016042 // lipid catabolic process // inferred from electronic annotation///0007586 // digestion
713.002 453.6092	0.005 NM_025606		-1.55 Mrpl16	mitochondrial ribosomal protein L16	0006412 // translation // inferred from electronic annotation///0006412 // translation // inferre
40.25615 25.29746	0.021 NM_013600///NM_0		-1.55 Msh5	mutS homolog 5 (E. coli)	0007292 // female gamete generation // inferred from mutant phenotype///0006986 // respon
75.99167 48.63821	0.018 NM_013848		-1.55 Ermap	erythroblast membrane-associated protein	0031410 // cytoplasmic vesicle // inferred from direct assay///0005886 // plasma membrane //
689.6768 432.4806	0.025 NM_139229		-1.55 Pdf///Cog8	peptide deformylase (mitochondrial)///component of oligomeric golgi cor	0006810 // transport // inferred from electronic annotation///0015031 // protein transport // ir
38.46425 24.01132	0.036 NM_009250		-1.55 Serpin1	Serine (or cysteine) peptidase inhibitor, clade I, member 1, mRNA (cDNA clone MGC:6413 IMAGE:3588856)///serine (or cysteine) peptidase inhibitor, clade I, member 1	0008092 // cytoskeletal protein binding // inferred from electronic annotation///0005488 // bin
310.948 198.2547	0.022 XM_980440///NM_0		-1.56 Epb4.1I4b	erythrocyte protein band 4.1-like 4b	0007264 // small GTPase mediated signal transduction // inferred from electronic annotation///
288.2301 181.93	0.029 NM_011227		-1.56 Rab20	RAB20, member RAS oncogene family	0006810 // transport // inferred from electronic annotation///0015031 // protein transport // ir
294.0204 184.8419	0.019 NM_001127191///NM		-1.56 Snx16	sorting nexin 16	0005739 // mitochondrion // inferred from electronic annotation///0030529 // ribonucleoprote
326.6604 204.8988	0.023 NM_178603		-1.56 Mrpl50	mitochondrial ribosomal protein L50	0016021 // integral to membrane // inferred from electronic annotation///0005739 // mitochor
1876.378 1180.146	0.015 NM_026618		-1.56 Ccdc56	coiled-coil domain containing 56	0017111 // nucleoside-triphosphatase activity // inferred from electronic annotation///0005524
424.6869 265.5952	0.047 NM_133823		-1.56 Mmaa	methylmalonic aciduria (cobalamin deficiency) type A	0051028 // mRNA transport // inferred from electronic annotation///0065002 // intracellular pr
292.9338 184.0178	0.014 NM_027091		-1.56 Nup35	nucleoporin 35	0046903 // secretion // inferred from direct assay///0045454 // cell redox homeostasis // infern
312.6984 197.4192	0.025 NM_133783		-1.56 Ptges2	prostaglandin E synthase 2	0043457 // regulation of cellular respiration // inferred from mutant phenotype
1636.327 1027.339	0.047 NM_134007		-1.56 Cisd1	CDGSH iron sulfur domain 1	
56.7785 36.335	0.035 NM_029610		-1.56 Lyrn1	LYR motif containing 1	
681.6025 428.0858	0.005 NM_024227		-1.57 Mrpl28	mitochondrial ribosomal protein L28	0045449 // regulation of transcription // inferred from electronic annotation
244.2457 153.2847	0.008 NM_001159612///NM		-1.57 Lrrc57	leucine rich repeat containing 57	0005515 // protein binding // inferred from electronic annotation
2692.067 1692.505	0.034 NM_025403		-1.57 Nop10	NOP10 ribonucleoprotein homolog (yeast)	0042254 // ribosome biogenesis // inferred from electronic annotation///0006364 // rRNA proc
296.6109 182.8616	0.045 NM_172575///NM_1		-1.57 Zfp277	zinc finger protein 277	0005515 // protein binding // inferred from electronic annotation///0008270 // zinc ion binding
132.542 83.09451	0.018 NM_029321		-1.57 Ttc32	tetratricopeptide repeat domain 32	0005488 // binding // inferred from electronic annotation

[ICR, PBS]([ICR, SUL])	p	RefSeq Transcript ID	FC [PBS:SFN]	Gene Symbol	Gene Title	Gene Ontology Biological Process
60.01769 37.55688	0.002	NM_145146	-1.58	Afm	afamin	0006810 // transport // inferred from electronic annotation
591.2401 365.0035	0.018	NM_177910	-1.58	Gmppb	GDP-mannose pyrophosphorylase B	0009058 // biosynthetic process // inferred from electronic annotation///0007157 // heterophil
640.9873 399.33	0.003	NM_027296	-1.59	Trnt1	tRNA nucleotidyl transferase, CCA-adding, 1	0008033 // tRNA processing // inferred from electronic annotation///0006396 // RNA processing
327.7994 200.8331	0.026	NM_026732	-1.59	Mrpl14	mitochondrial ribosomal protein L14///Mitochondrial ribosomal protein L1	0006412 // translation // inferred from electronic annotation
63.00163 38.51973	0.029	NM_026161	-1.59	C1qtnf4	C1q and tumor necrosis factor related protein 4, mRNA (cDNA clone IMAGE:3668760)///C1q and tumor necrosis factor related protein 4	0005739 // mitochondrion // inferred from electronic annotation///0005743 // mitochondrial in
1810.035 1128.829	0.022	NM_018819	-1.59	Brp44l	brain protein 44-like	0006412 // translation // inferred from electronic annotation///0006810 // transport // inferred
1139.32 703.316	0.014	NM_025450	-1.60	Mrps17	mitochondrial ribosomal protein S17	0006546 // glycine catabolic process // inferred from electronic annotation
1642.731 998.7895	0.050	NM_026572	-1.60	Gcsh	glycine cleavage system protein H (aminomethyl carrier)	0005515 // protein binding // inferred from electronic annotation
109.1562 68.12119	0.017	XM_908231///XM_85	-1.60	Lrrc51	leucine rich repeat containing 51	
87.10313 53.09328	0.029	XR_032922///NM_02	-1.60	Ppcs///EG667114	phosphopantothenoylcysteine synthetase///predicted gene, EG667114	
1018.958 629.4298	0.023	NM_026631	-1.60	Nhp2	NHP2 ribonucleoprotein homolog (yeast)	0042254 // ribosome biogenesis // inferred from electronic annotation///0031118 // rRNA pseu
177.6615 108.6985	0.022	NM_028836	-1.60	Ctbs	chitinase, di-N-acetyl-	0008152 // metabolic process // inferred from electronic annotation///0005975 // carbohydrate
860.6187 525.7906	0.006	NM_146165	-1.60	Jtv1	JTV1 gene	0006412 // translation // inferred from electronic annotation
3141.626 1913.345	0.018	NM_023202	-1.61	Ndufa7	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (B14.5a) (Ndufa7)	0042773 // ATP synthesis coupled electron transport // inferred from electronic annotation///00
2050.234 1245.538	0.031	NM_019745	-1.61	Pdcd10	programmed cell death 10	0006915 // apoptosis // inferred from electronic annotation
408.1969 252.0951	0.006	NM_001142681///NM	-1.61	Chid1	chitinase domain containing 1	0005975 // carbohydrate metabolic process // inferred from electronic annotation///0006032 //
605.7777 366.1319	0.048	NM_133679	-1.62	Cryz1	crystallin, zeta (quinone reductase)-like 1	0055114 // oxidation reduction // inferred from electronic annotation///0008152 // metabolic p
118.8187 71.68528	0.014	NM_001039534	-1.62	Pstk	phosphoserine-tRNA kinase	0006412 // translation // inferred from electronic annotation///0006355 // regulation of transcr
53.58475 33.25836	0.038	NM_007755	-1.62	Cpeb1	cytoplasmic polyadenylation element binding protein 1	0007130 // synaptonemal complex assembly // inferred from mutant phenotype///0006417 // r
737.2197 437.0958	0.043	NM_009069	-1.62	Rit1	Ras-like without CAAX 1	0007264 // small GTPase mediated signal transduction // inferred from electronic annotation
373.2211 226.2109	0.013	NM_026448	-1.63	Klhl7	kelch-like 7 (Drosophila)	0005515 // protein binding // inferred from electronic annotation
1017.697 614.6252	0.013	NM_175277	-1.63	Bola3	bolA-like 3 (E. coli)	
576.665 347.6554	0.015	NM_026452	-1.63	Coq9	coenzyme Q9 homolog (yeast)	0006744 // ubiquinone biosynthetic process // inferred from electronic annotation
218.0706 130.0511	0.013	NM_029629	-1.64	Fahd2a	fumarylacetoacetate hydrolase domain containing 2A	0008152 // metabolic process // inferred from electronic annotation
1010.362 599.4307	0.033	NM_025798	-1.64	Hint3	histidine triad nucleotide binding protein 3	0016787 // hydrolase activity // inferred from electronic annotation///0003824 // catalytic activ
7552.051 4567.932	0.004	NM_028618///NM_1	-1.64	Dmkn	dermokine	0030154 // cell differentiation // inferred from electronic annotation
446.1181 266.0846	0.029	NM_026526	-1.64	N6amt2	N-6 adenine-specific DNA methyltransferase 2 (putative)	0032259 // methylation // inferred from electronic annotation
4272.006 2531.228	0.044	NM_025983	-1.64	Atp5e	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit	0015992 // proton transport // inferred from electronic annotation///0015986 // ATP synthesis
49.65157 29.80688	0.023	NM_144943	-1.64	Cd207	CD207 antigen	0005529 // sugar binding // inferred from electronic annotation///0005488 // binding // inferre
126.8392 75.34242	0.025	XM_001473278///NM	-1.64	LOC100044896///Scdp	saccharopine dehydrogenase (putative)///similar to Saccharopine dehydro	0055114 // oxidation reduction // inferred from electronic annotation///0008152 // metabolic p
102.178 61.38092	0.008	NM_009544	-1.65	Zfp105	zinc finger protein 105	0008270 // zinc ion binding // inferred from electronic annotation///0003676 // nucleic acid bin
644.2593 377.8097	0.030	NM_001033297	-1.65	Gm561	gene model 561, (NCBI)	
654.8452 384.9943	0.050	NM_027925	-1.65	Trnau1ap	tRNA selenocysteine 1 associated protein 1	0006412 // translation // inferred from electronic annotation///0001514 // selenocysteine incor
560.3851 332.4734	0.031	NM_207625///NM_0	-1.66	Acs14	acyl-CoA synthetase long-chain family member 4	0008152 // metabolic process // inferred from electronic annotation///0019217 // regulation of
43.55812 25.82665	0.001	XR_002074///XR_033	-1.66	LOC674137///LOC6766	similar to RT1 class I histocompatibility antigen, AA alpha chain precursor///	0002474 // antigen processing and presentation of peptide antigen via MHC class I // inferred fr
362.2102 211.3004	0.014	NM_001012400	-1.67	AU022252	expressed sequence AU022252	
140.0045 82.49772	0.034	NM_001080820///NM	-1.67	Cass4	Cas scaffolding protein family member 4	0007155 // cell adhesion // inferred from electronic annotation
305.6148 178.4218	0.024	NM_001004190	-1.67	Zfp560	zinc finger protein 560	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation//
1170.233 669.1027	0.045	NM_001031808	-1.67	Mrpl41	mitochondrial ribosomal protein L41	0006915 // apoptosis // inferred from electronic annotation///0007049 // cell cycle // inferred f
641.6351 378.3987	0.006	NM_026392///NM_0	-1.68	Tmem70	transmembrane protein 70	0033615 // mitochondrial proton-transporting ATP synthase complex assembly // inferred from
765.8442 447.9453	0.043	NM_018820	-1.68	Sertad1	SERTA domain containing 1	0030308 // negative regulation of cell growth // not recorded///0006355 // regulation of transcr
2987.745 1744.462	0.009	NM_012021	-1.68	Prdx5	peroxiredoxin 5	0055114 // oxidation reduction // inferred from electronic annotation///0045454 // cell redox h
328.4195 194.028	0.012	NM_001130149///NM	-1.68	LOC100045148///Rnas	ribonuclease III, nuclear///similar to ribonuclease III, nuclear	0006396 // RNA processing // inferred from electronic annotation
223.5362 127.8515	0.036	NR_003946///NM_02	-1.68	Hyi	hydroxyypyruvate isomerase homolog (E. coli)	0008903 // hydroxyypyruvate isomerase activity // inferred from electronic annotation///001685
145.3545 86.19986	0.033	NM_022986	-1.69	Irak1bp1	interleukin-1 receptor-associated kinase 1 binding protein 1	0007249 // I-kappaB kinase/NF-kappaB cascade // inferred from direct assay///0006355 // regul
138.8898 80.59638	0.018	NM_001082412///NM	-1.69	Mcart6	mitochondrial carrier triple repeat 6	0006810 // transport // inferred from electronic annotation
477.323 278.0555	0.007	NM_019752	-1.70	Htra2	Htra serine peptidase 2	0006915 // apoptosis // inferred from electronic annotation///0008629 // induction of apoptosi
237.1729 136.5268	0.027	XM_001473278///NM	-1.70	LOC100044896///Scdp	saccharopine dehydrogenase (putative)///similar to Saccharopine dehydro	0055114 // oxidation reduction // inferred from electronic annotation///0008152 // metabolic p
158.613 91.81495	0.009	NM_029612	-1.70	Slamf9	SLAM family member 9	0016021 // integral to membrane // inferred from electronic annotation///0016020 // membrar
23.96309 13.79724	0.041	NM_001077353///NM	-1.70	Gsta3	glutathione S-transferase, alpha 3	0008152 // metabolic process // inferred from electronic annotation
455.092 262.7985	0.002	NM_025554	-1.71	Polr2e	polymerase (RNA) II (DNA directed) polypeptide E	0006350 // transcription // inferred from electronic annotation
497.4266 284.8073	0.001	NR_003518///XR_035	-1.72	D030013116Rik///Pisd	phosphatidylserine decarboxylase, pseudogene 1///RIKEN cDNA D0300131	0008654 // phospholipid biosynthetic process // inferred from electronic annotation
320.0594 180.3527	0.026	NM_172254///NM_0	-1.72	Dph3	DPH3 homolog (KT11, S. cerevisiae)	0051099 // positive regulation of binding // inferred from sequence or structural similarity///000
36.50731 20.76711	0.038	NM_134160	-1.72	Mcoln3	mucolipin 3	0006811 // ion transport // inferred from electronic annotation///0006810 // transport // infer
1482.056 832.7785	0.025	NM_145517	-1.72	Ormdl1	ORM1-like 1 (S. cerevisiae)	0006508 // proteolysis // inferred from electronic annotation
758.034 439.0158	0.039	NM_138721	-1.73	Lsm10	U7 snRNP-specific Sm-like protein LSM10	0006398 // histone mRNA 3'-end processing // traceable author statement///0008380 // RNA sp
637.9747 361.2487	0.001	NR_003518///XR_035	-1.74	D030013116Rik///Pisd	phosphatidylserine decarboxylase, pseudogene 1///RIKEN cDNA D0300131	0008654 // phospholipid biosynthetic process // inferred from electronic annotation
341.7427 194.705	0.003	NM_029985	-1.74	Lrrc42	leucine rich repeat containing 42	
1848.543 1059.303	0.018	XM_001481167///XN	-1.74	Tmem181///Dynlt1d//	transmembrane protein 181///dynein light chain Tctex-type 1D///dynein li	0007017 // microtubule-based process // inferred from direct assay
219.636 121.295	0.032	NM_032003	-1.74	Enpp5	ectonucleotide pyrophosphatase/phosphodiesterase 5	0009166 // nucleotide catabolic process // not recorded///0008152 // metabolic process // infer

[ICR, PBS]([ICR, SUL])p	RefSeq Transcript ID	FC [PBS:SFN]	Gene Symbol	Gene Title	Gene Ontology Biological Process
1129.348 644.199	0.006 NM_053119	-1.74	Echs1	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial	0008152 // metabolic process // inferred from electronic annotation///0006629 // lipid metabo
2764.42 1578.652	0.018 XM_001481167///XM	-1.75	Dynl1d1///Dynl11///E	dynein light chain Tctex-type 1D///dynein light chain Tctex-type 1///predic	0007017 // microtubule-based process // inferred from direct assay
20.48614 11.37225	0.015 NM_173422	-1.75	Colec10	collectin sub-family member 10	0009790 // embryonic development // non-traceable author statement///0006952 // defense re
392.2964 216.2384	0.032 NM_011765///NM_0	-1.75	BC018101///Zfp97	zinc finger protein 97///cDNA sequence BC018101	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation//
257.9928 146.3981	0.040 NM_023196///NM_1	-1.76	Pla2g12a	phospholipase A2, group XIIA	0006644 // phospholipid metabolic process // inferred from electronic annotation///0016042 //
85.22612 48.56184	0.014 NM_027208	-1.76	Bdh2	3-hydroxybutyrate dehydrogenase, type 2	0055114 // oxidation reduction // inferred from electronic annotation///0008152 // metabolic p
100.7416 55.61209	0.034 NM_025476	-1.76	Fam82b	family with sequence similarity 82, member B	0005488 // binding // inferred from electronic annotation
684.1805 374.7329	0.020 NM_016763	-1.77	Hsd17b10	hydroxysteroid (17-beta) dehydrogenase 10	0055114 // oxidation reduction // inferred from electronic annotation///0008152 // metabolic p
75.45448 41.3073	0.031 NM_008281///NM_0	-1.77	Hpn	hepsin	0016049 // cell growth // inferred from electronic annotation///0006508 // proteolysis // inferri
312.5625 175.3697	0.004 NM_133768	-1.78	Asl	argininosuccinate lyase	0000053 // argininosuccinate metabolic process // inferred from electronic annotation///00196
668.3716 362.148	0.036 NM_008403	-1.78	Itgb1bp1	integrin beta 1 binding protein 1	0030155 // regulation of cell adhesion // not recorded///0007160 // cell-matrix adhesion // infe
219.8164 119.9206	0.018 NM_027175	-1.78	Ndufaf1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 1	0008137 // NADH dehydrogenase (ubiquinone) activity // inferred from electronic annotation
311.9056 167.5919	0.030 NM_026816	-1.78	Gtf2f2	general transcription factor IIF, polypeptide 2	0045944 // positive regulation of transcription from RNA polymerase II promoter // inferred fro
153.3364 84.44883	0.011 NM_010210	-1.78	Fhit	fragile histidine triad gene	0009117 // nucleotide metabolic process // traceable author statement///0006260 // DNA repli
123.403 69.23351	0.050 NM_182783	-1.80	Fam167b	family with sequence similarity 167, member B	
130.9017 70.01032	0.023 NM_016746///NM_0	-1.80	Ccnc	cyclin C	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation//
181.0848 96.50521	0.029 NM_026908	-1.80	Cab39l	Calcium binding protein 39-like, mRNA (cDNA clone MGC:27972 IMAGE:35	0005488 // binding // inferred from electronic annotation
143.07 76.97679	0.029 NM_008521	-1.80	Ltc4s	leukotriene C4 synthase	0006691 // leukotriene metabolic process // inferred from electronic annotation///0006691 // l
57.41704 31.49134	0.016 NM_013542	-1.81	Gzmb	granzyme B	0006915 // apoptosis // inferred from electronic annotation///0019835 // cytolysis // inferred fr
922.3467 501.9294	0.000 NM_008655	-1.81	Gadd45b	Growth arrest and DNA-damage-inducible 45 beta, mRNA (cDNA clone MG	0051726 // regulation of cell cycle // inferred from direct assay///0006915 // apoptosis // inferri
342.9352 184.2806	0.005 NM_023175	-1.82	Nit2	nitrilase family, member 2	0006807 // nitrogen compound metabolic process // inferred from electronic annotation
465.5807 248.5234	0.017 NM_025351	-1.82	Chcd6	coiled-coil-helix-coiled-coil-helix domain containing 6	
2220.494 1160.979	0.037 NM_028260	-1.82	Immp1l	IMP1 inner mitochondrial membrane peptidase-like (S. cerevisiae)	0008236 // serine-type peptidase activity // inferred from electronic annotation///0016787 // h
2157.829 1148.805	0.029 NM_026752	-1.82	Zfyve21	zinc finger, FYVE domain containing 21	0046872 // metal ion binding // inferred from electronic annotation///0008270 // zinc ion bindi
60.59875 32.02939	0.024 NM_001038654///NM	-1.83	Slc16a3	solute carrier family 16 (monocarboxylic acid transporters), member 3	0015711 // organic anion transport // inferred from electronic annotation///0006810 // transpo
65.25829 35.06831	0.001 NM_019686	-1.84	Cib2	calcium and integrin binding family member 2	0007229 // integrin-mediated signaling pathway // inferred from electronic annotation
101.9652 54.32904	0.015 NM_023900	-1.84	Plekhd1	pleckstrin homology domain containing, family J member 1	0005515 // protein binding // inferred from electronic annotation
348.9084 184.2331	0.010 NM_026981	-1.84	Dtw1	DTW domain containing 1	
20.37019 10.75001	0.005 NM_013930	-1.86	Aass	aminoadipate-semialdehyde synthase	0055114 // oxidation reduction // inferred from electronic annotation///0008152 // metabolic p
418.7346 221.8955	0.000 NM_028053	-1.87	Tmem38b	transmembrane protein 38B///Transmembrane protein 38B (Tmem38b), n	0006813 // potassium ion transport // inferred from electronic annotation///0006811 // ion tra
313.7644 164.9038	0.025 NM_026465	-1.88	Ncrna00117	non-protein coding RNA 117	
775.4144 398.2403	0.023 NM_025654	-1.89	Rdm1	RAD52 motif 1	0003677 // DNA binding // inferred from electronic annotation///0003723 // RNA binding // infe
280.8091 144.5645	0.007 NM_016918	-1.90	Nudt5	nudix (nucleoside diphosphate linked moiety X)-type motif 5	0006139 // nucleobase, nucleoside, nucleotide and nucleic acid metabolic process // inferred fr
195.6902 102.7243	0.036 NM_019487	-1.91	Hebp2	heme binding protein 2	0005737 // cytoplasm // inferred from direct assay///0005737 // cytoplasm // inferred from ele
95.06571 48.2388	0.024 NM_028051///NM_0	-1.91	Slc39a5	solute carrier family 39 (metal ion transporter), member 5	0006829 // zinc ion transport // traceable author statement///0030001 // metal ion transport //
92.20453 46.38475	0.019 NM_013754	-1.91	Ins16	insulin-like 6	0005179 // hormone activity // inferred from electronic annotation
77.01664 39.70833	0.019 NM_011196	-1.92	Ptger3	prostaglandin E receptor 3 (subtype EP3)	0015701 // bicarbonate transport // inferred from mutant phenotype///0007165 // signal trans
58.40881 28.69086	0.037 NM_011760	-1.94	Zfp54	zinc finger protein 54	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation//
134.536 64.73121	0.033 XM_194572///NM_0	-1.96	Etoh1	ethanol induced 1	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation//
1034.297 528.4978	0.046 NM_008536	-1.96	Tm4sf1	transmembrane 4 superfamily member 1	0005887 // integral to plasma membrane // inferred from electronic annotation///0016021 // in
611.846 311.8536	0.033 NM_009222	-1.97	Snap23	synaptosomal-associated protein 23	0006810 // transport // inferred from electronic annotation///0015031 // protein transport // ir
106.3862 50.90015	0.025 NM_029942	-2.00	Prelid2	PRELI domain containing 2	
222.2006 105.0448	0.035 NM_025429	-2.03	Serpinb1a	serine (or cysteine) peptidase inhibitor, clade B, member 1a	0042176 // regulation of protein catabolic process // inferred from physical interaction
75.25092 36.97152	0.027 NM_009014	-2.04	Rad51l1	RAD51-like 1 (S. cerevisiae)	0006974 // response to DNA damage stimulus // inferred from electronic annotation///0006310
657.9487 321.7397	0.007 NM_026347	-2.06	Iah1	isoamyl acetate-hydrolyzing esterase 1 homolog (S. cerevisiae)	0016042 // lipid catabolic process // inferred from electronic annotation///0006629 // lipid met
217.3756 99.474	0.021 NM_010893	-2.08	Neu1	neuraminidase 1	0008152 // metabolic process // inferred from electronic annotation
45.13906 21.32257	0.002 XR_002074///XR_033	-2.10	LOC674137///LOC676	similar to RT1 class I histocompatibility antigen, AA alpha chain precursor/	0002474 // antigen processing and presentation of peptide antigen via MHC class I // inferred fr
433.5234 191.1205	0.044 NM_175095	-2.12	Comm2	COMM domain containing 2	0005515 // protein binding // inferred from electronic annotation
119.4844 54.20826	0.024 NM_023523	-2.13	Pecr	peroxisomal trans-2-enoyl-CoA reductase	0055114 // oxidation reduction // inferred from electronic annotation///0008152 // metabolic p
25.80614 11.38525	0.032 NM_010391	-2.14	H2-Q10	histocompatibility 2, Q region locus 10	0002474 // antigen processing and presentation of peptide antigen via MHC class I // inferred fr
899.5041 416.2256	0.022 NM_025273	-2.18	Pcbd1	pterin 4 alpha carbinolamine dehydratase/dimerization cofactor of hepato	0043496 // regulation of protein homodimerization activity // inferred from direct assay///0051
58.36729 26.84178	0.011 NM_018746///NM_0	-2.19	Itih4	inter alpha-trypsin inhibitor, heavy chain 4	0030212 // hyaluronan metabolic process // inferred from electronic annotation
509.9585 221.1738	0.047 NM_007994	-2.27	Fbp2	fructose biphosphatase 2	0005975 // carbohydrate metabolic process // inferred from electronic annotation///0006094 //
175.9481 76.97847	0.030 NM_029556	-2.29	Clybl	citrate lyase beta like	0006725 // cellular aromatic compound metabolic process // inferred from electronic annotatio
45.35812 17.94804	0.050 NM_020049	-2.35	Slc6a14	solute carrier family 6 (neurotransmitter transporter), member 14	0006865 // amino acid transport // inferred from electronic annotation///0006836 // neurotran
147.2613 61.84474	0.037 NM_009437	-2.36	Tst	thiosulfate sulfurtransferase, mitochondrial	0008272 // sulfate transport // inferred from electronic annotation
887.5344 359.9771	0.018 NM_027299	-2.37	Degs2	degenerative spermatocyte homolog 2 (Drosophila), lipid desaturase	0055114 // oxidation reduction // inferred from electronic annotation///0006629 // lipid metab
283.5951 114.1662	0.012 NM_033612	-2.38	cela1	chymotrypsin-like elastase family, member 1	0006508 // proteolysis // inferred from electronic annotation
295.7775 128.9315	0.047 NM_030004	-2.40	Cryl1	crystallin, lambda b1	0055114 // oxidation reduction // inferred from electronic annotation///0008152 // metabolic p
98.13062 39.13979	0.048 NM_031198	-2.47	Tcfec	transcription factor EC	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation//

[ICR, PBS]([ICR, SUL])p	RefSeq Transcript ID	FC [PBS:SFN]	Gene Symbol	Gene Title	Gene Ontology Biological Process
959.7819 372.2889	0.026 NM_001102468///NM	-2.48	<i>Calml4</i>	calmodulin-like 4	0005509 // calcium ion binding // inferred from electronic annotation
82.68385 30.72629	0.015 NM_008964	-2.54	<i>Ptger2</i>	prostaglandin E receptor 2 (subtype EP2)	0042127 // regulation of cell proliferation // inferred from genetic interaction///0007165 // sign
237.3564 96.25427	0.028 NM_025393	-2.58	<i>S100a14</i>	S100 calcium binding protein A14	0005509 // calcium ion binding // inferred from electronic annotation
297.5703 110.8488	0.030 NM_183136	-2.68	<i>Spink8</i>	serine peptidase inhibitor, Kazal type 8	0004866 // endopeptidase inhibitor activity // inferred from electronic annotation///0004867 //
159.78 55.80623	0.039 NM_007443	-2.72	<i>Ambp</i>	alpha 1 microglobulin/bikunin	0018298 // protein-chromophore linkage // inferred from electronic annotation///0006810 // tr
102.0721 34.39528	0.035 NM_030601///NM_0	-2.75	<i>Clca1///Clca2</i>	chloride channel calcium activated 1///chloride channel calcium activated	0006915 // apoptosis // inferred from direct assay///0006821 // chloride transport // inferred fr
236.1969 86.81435	0.046 NM_007428	-2.76	<i>Agt</i>	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	0001999 // renal response to blood flow during renin-angiotensin regulation of systemic arterial
190.6407 62.39538	0.045 NM_026680	-2.86	<i>Golt1a</i>	golgi transport 1 homolog A (S. cerevisiae)	0006810 // transport // inferred from electronic annotation///0016192 // vesicle-mediated tran
277.9861 94.95822	0.014 NM_054098	-2.88	<i>Steap4</i>	STEAP family member 4	0045444 // fat cell differentiation // inferred from expression pattern///0055114 // oxidation re
80.82946 25.35468	0.025 NM_030703	-2.92	<i>Cpn1</i>	carboxypeptidase N, polypeptide 1	0006508 // proteolysis // inferred from electronic annotation
1170.563 416.8855	0.014 NM_010373	-2.95	<i>Gzme</i>	granzyme E	0019835 // cytolysis // inferred from electronic annotation///0006508 // proteolysis // inferred
135.4999 48.5519	0.030 NM_177372	-2.99	<i>Dna2</i>	DNA replication helicase 2 homolog (yeast)	0006260 // DNA replication // inferred from electronic annotation
1166.445 422.6965	0.041 NM_133900	-3.02	<i>Psph</i>	phosphoserine phosphatase	0008152 // metabolic process // inferred from electronic annotation///0008652 // amino acid b
124.829 43.1871	0.025 NM_010371	-3.05	<i>Gzmc</i>	granzyme C	0019835 // cytolysis // inferred from electronic annotation///0006508 // proteolysis // inferred
235.968 70.08734	0.028 NM_030601///NM_0	-3.14	<i>Clca1///Clca2</i>	chloride channel calcium activated 1///chloride channel calcium activated	0006915 // apoptosis // inferred from direct assay///0006821 // chloride transport // inferred fr
468.7179 147.8166	0.018 NM_008969	-3.15	<i>Ptgs1</i>	prostaglandin-endoperoxide synthase 1	0042127 // regulation of cell proliferation // inferred from genetic interaction///0006979 // resq
624.2955 165.2511	0.045 NM_009393	-3.47	<i>Tnnc1</i>	troponin C, cardiac/slow skeletal	0060048 // cardiac muscle contraction // inferred from electronic annotation///0055010 // vent
510.1474 144.6265	0.008 NM_010374	-3.59	<i>Gzmf</i>	granzyme F	0019835 // cytolysis // inferred from electronic annotation///0006508 // proteolysis // inferred
3432.359 973.1182	0.039 NM_008557	-3.74	<i>Fxyd3</i>	FX1D domain-containing ion transport regulator 3	0006811 // ion transport // inferred from electronic annotation///0006810 // transport // infer
76.90684 18.04546	0.048 NM_031197	-3.74	<i>Slc2a2</i>	solute carrier family 2 (facilitated glucose transporter), member 2	0015758 // glucose transport // inferred from electronic annotation///0055085 // transmembra
155.0606 44.29022	0.040 XM_001475511///NM	-3.77	<i>Mosc1///LOC1000459</i>	MOCO sulphurase C-terminal domain containing 1///similar to MOSC dom	0055114 // oxidation reduction // inferred from electronic annotation
65.23593 15.47273	0.015 NM_009996	-3.79	<i>Cyp24a1</i>	cytochrome P450, family 24, subfamily a, polypeptide 1	0042359 // vitamin D metabolic process // inferred from mutant phenotype///0055114 // oxida
867.3882 233.5265	0.004 NM_008341	-3.86	<i>Igfbp1</i>	insulin-like growth factor binding protein 1	0001558 // regulation of cell growth // inferred from electronic annotation
769.3154 204.8184	0.012 NM_010375	-3.89	<i>Gzmg</i>	granzyme G	0019835 // cytolysis // inferred from electronic annotation///0006508 // proteolysis // inferred
541.9498 110.5021	0.045 NM_010361	-3.94	<i>Gstt2</i>	glutathione S-transferase, theta 2	0006749 // glutathione metabolic process // not recorded///0006749 // glutathione metabolic p
1153.052 308.8997	0.014 NM_010372	-4.11	<i>Gzmd</i>	granzyme D	0019835 // cytolysis // inferred from electronic annotation///0006508 // proteolysis // inferred
125.4495 26.23067	0.006 NM_008185	-4.43	<i>Gstt1</i>	glutathione S-transferase, theta 1	0006749 // glutathione metabolic process // inferred from direct assay
135.9316 18.1094	0.047 NM_019395	-5.20	<i>Fbp1</i>	fructose biphosphatase 1	0005975 // carbohydrate metabolic process // inferred from electronic annotation///0006094 //
289.3531 43.62996	0.049 NM_019545	-5.37	<i>Hao3</i>	hydroxyacid oxidase (glycolate oxidase) 3	0055114 // oxidation reduction // inferred from electronic annotation///0008152 // metabolic p
201.1406 24.84246	0.000 NM_010701	-7.84	<i>Lect1</i>	leukocyte cell derived chemotaxin 1	0007275 // multicellular organismal development // inferred from electronic annotation///0045
475.6654 25.90099	0.030 NM_025658	-13.01	<i>Ms4a4d</i>	membrane-spanning 4-domains, subfamily A, member 4D	0007165 // signal transduction // inferred from electronic annotation
498.221 31.61247	0.000 XR_032349///NM_01	-16.14	<i>H2-L///LOC636948///H</i>	histocompatibility 2, D region locus 1///similar to H-2 class I histocompatib	0051289 // protein homotetramerization // inferred from direct assay///0006952 // defense res
2475.117 17.70803	0.001 NM_021475	-109.27	<i>Adamdec1</i>	ADAM-like, decysin 1	0006508 // proteolysis // inferred from electronic annotation

Table S6. Prenatal sulforaphane-modulated genes in *Nrf2*^{-/-} placenta (T Test unpaired p-value P <= 0.05)

>=1.5-fold 367 genes

RIKEN cDNA and predicted genes excluded. Fold Change (FC): Blue (-) - fold lower in SFN than PBS, Red - fold higher in SFN than PBS.

Genes altered by SFN in common in *Nrf2*-WT and -KO placenta.

[Nrf2-KO, PBS]([Nrf2-KO, SFN] p	RefSeq Transcript ID	FC PBS:SFN	Gene Symbol	Gene Title	Gene Ontology
29.654598	139.6766	0.002 NM_010701///XM_0065	4.71 Lct1	leukocyte cell derived chemotaxin 1	0001886 // endothelial cell morphogenesis // inferred from direct assay///0001937 // negative re
100.55591	290.45444	0.001 NM_001081212	2.89 Irs2	insulin receptor substrate 2	0002053 // positive regulation of mesenchymal cell proliferation // inferred from genetic interact
45.319675	106.36528	0.003 NM_008634///XM_0065	2.35 Map1b	microtubule cytoskeleton organization	0000226 // microtubule cytoskeleton organization // inferred from electronic annotation///00001
92.82944	209.91774	0.006 NM_009706///XM_0065	2.26 Arhgap5	Rho GTPase activating protein 5	0002053 // positive regulation of mesenchymal cell proliferation // inferred from mutant phenot
1987.436	4424.0757	0.002 NM_013724///XM_0065	2.23 Nrk	Nik related kinase	0006468 // protein phosphorylation // not recorded///0007256 // activation of JNKK activity // in
17.585354	38.495815	0.000 NM_011670	2.19 Uchl1	ubiquitin carboxy-terminal hydrolase L1	0002931 // response to ischemia // inferred from mutant phenotype///0006508 // proteolysis //
107.7787	232.66904	0.007 NM_133249///XM_0065	2.16 Ppargc1b	peroxisome proliferative activated receptor, gamma, coactivator 1 beta	0001503 // ossification // inferred from mutant phenotype///0006351 // transcription, DNA-tem
86.64082	184.87636	0.003 NM_001159603///NM_C	2.13 Pum1	pumilio RNA-binding family member 1	0006417 // regulation of translation // inferred from electronic annotation
198.3993	410.63806	0.006 NM_001033167///XM_0	2.07 Slc22a23	solute carrier family 22, member 23	0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferre
183.62709	373.68777	0.003 NM_001081395///XM_0	2.04 Amot1	angiomin-like 1	0003365 // establishment of cell polarity involved in ameboidal cell migration // inferred from mu
236.45654	466.55453	0.002 NM_013813///XM_0065	1.97 Epb4.113	erythrocyte protein band 4.1-like 3	0002175 // protein localization to paranode region of axon // inferred from mutant phenotype///
224.81752	438.51678	0.001 NM_023598///XM_0065	1.95 Arid5b	AT rich interactive domain 5B (MRF1-like)	0001822 // kidney development // inferred from mutant phenotype///0006351 // transcription, l
31.940857	61.276947	0.006 NM_019496	1.92 Ammcr1	Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region gene 1	
78.55106	150.46126	0.002 NM_027707///NM_2012	1.92 Nipbl	Nipped-B homolog (Drosophila)	
236.47023	451.6383	0.005 NM_001033422///XM_0	1.91 Thoc2	THO complex 2	
150.81491	284.48697	0.001 NM_033563///XM_0064	1.89 Klf7	Kruppel-like factor 7 (ubiquitous)	
546.5554	1022.07465	0.001 NM_009320///XM_0065	1.87 Slc6a6	solute carrier family 6 (neurotransmitter transporter, taurine), member 6	
259.63635	485.46533	0.009 NM_175229///XM_0065	1.87 Srrm2	serine/arginine repetitive matrix 2	
212.05516	392.16537	0.002 NM_026666///XM_0065	1.85 Ubn1	ubinnuclein 1	
275.78058	508.23175	0.007 NM_001166584///NM_C	1.84 Tead1	TEA domain family member 1	
466.95718	856.161	0.000 NM_010638	1.83 Klf9	Kruppel-like factor 9	
213.48146	389.41882	0.001 NM_008448	1.82 Kif5b	kinesin family member 5B	
268.03125	487.97748	0.002 NM_00110826///NM_C	1.82 Ddx6	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6	
297.5103	537.5202	0.003 NM_009367///XM_0064	1.81 Tgfb2	transforming growth factor, beta 2	
116.7948	208.21835	0.001 NM_010559///XM_0065	1.78 Il6ra	interleukin 6 receptor, alpha	
325.14688	579.4461	0.001 NM_023275	1.78 Rhoj	Ras homolog gene family, member J	
146.65102	259.05176	0.002 NM_008306///XM_0065	1.77 Ndst1	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	
60.01903	105.209496	0.003 NM_177628///XM_0065	1.75 Fam167a	family with sequence similarity 167, member A	
117.15238	205.0593	0.004 NM_001037221///NM_C	1.75 Samd4	sterile alpha motif domain containing 4	
86.87219	151.83783	0.000 NM_153542///XM_0065	1.75 Lrrc20	leucine rich repeat containing 20	
290.54257	505.5732	0.006 NM_011595	1.74 Timp3	tissue inhibitor of metalloproteinase 3	
221.74672	385.83133	0.003 NM_010415	1.74 Hbegf	heparin-binding EGF-like growth factor	
60.15734	104.51836	0.003 NM_001025572///XM_0	1.74 Ankrd12	ankyrin repeat domain 12	
445.643	771.2975	0.007 NM_009149	1.73 Glg1	golgi apparatus protein 1	
242.51205	417.68323	0.001 NM_010612	1.72 Kdr	kinase insert domain protein receptor	
29.918562	51.37372	0.001 NM_133829///NM_178C	1.72 Mfsd6	major facilitator superfamily domain containing 6	
153.77072	263.67532	0.004 NM_020181///XM_0065	1.71 Fam129a	family with sequence similarity 129, member A	
138.10278	236.51712	0.004 NM_027045///NM_0284	1.71 Ccser2	coiled-coil serine rich 2	
148.1518	253.30557	0.009 NM_001024955///NM_C	1.71 Pik3r1	phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 1 (p85 alpha)	
48.484287	82.86876	0.001 NM_009179///XM_0065	1.71 St3gal2	ST3 beta-galactoside alpha-2,3-sialyltransferase 2	
31.0933	52.967587	0.002 NM_010216///XM_0065	1.70 Figf	c-fos induced growth factor	
686.9339	1166.1697	0.006 NM_001286944///NM_C	1.70 Jund	jun D proto-oncogene	
29.975426	50.643105	0.002 NM_172806///XM_0065	1.69 Btdb7	BTB (POZ) domain containing 7	
646.1344	1089.8871	0.000 NM_001035532///NM_C	1.69 Akap2	A kinase (PRKA) anchor protein 2	
163.66634	275.7104	0.003 NM_001289895///NM_C	1.68 Tns1	tensin 1	
55.71182	93.38969	0.008 NM_026083///NM_0273	1.68 Zc3h13	zinc finger CCHC type containing 13	
470.6281	787.2458	0.006 NM_175260///XM_0065	1.67 Myh10	myosin, heavy polypeptide 10, non-muscle	
74.19704	123.851494	0.007 NM_001081345	1.67 Chd2	chromodomain helicase DNA binding protein 2	
183.03212	304.75214	0.007 NM_173863///XM_0065	1.67 Crtc3	CREB regulated transcription coactivator 3	
258.22665	429.66727	0.002 NM_018868///XM_0064	1.66 Naps58	NOP58 ribonucleoprotein	
139.32092	231.62354	0.003 NM_001085472///NM_C	1.66 Acin1	apoptotic chromatin condensation inducer 1	
783.2815	1300.5016	0.003 NM_019764///XM_0065	1.66 Amotl2	angiomin-like 2	
123.759094	205.37727	0.006 NM_019827///XM_0065	1.66 Gsk3b	glycogen synthase kinase 3 beta	
101.437164	167.71692	0.006 NM_001081290///XM_0	1.65 Prrc2c	proline-rich coiled-coil 2C	
91.79746	151.67366	0.003 NM_175375///NM_2012	1.65 Ankhd1///Elf4ebp3///Masf	ankyrin repeat and KH domain containing 1///eukaryotic translation initiation factor 4E binding protein 3///m	
51.99767	85.33215	0.002 NM_001081308///NM_C	1.64 Taok3	TAO kinase 3	
24.316162	39.710747	0.003 NM_007731///XM_0065	1.63 Col13a1	collagen, type XIII, alpha 1	
138.46472	226.06395	0.001 NM_009125///XM_0065	1.63 Atxn2	ataxin 2	
114.34457	186.64891	0.002 NM_172627///XM_0065	1.63 Pgg11b	protein geranylgeranyltransferase type I, beta subunit	
852.8893	1386.0612	0.007 NM_010515	1.63 Igf2r	insulin-like growth factor 2 receptor	
100.08163	162.52353	0.000 NM_016670///NR_0274	1.62 Pknax1	Pbx/knotted 1 homeobox	
30.79821	49.81701	0.004 NM_009022	1.62 Aldh1a2	aldehyde dehydrogenase family 1, subfamily A2	
1311.2756	2117.584	0.002 NM_001198949///NM_C	1.61 Ralbp1	ralA binding protein 1	
436.66263	704.89874	0.005 NM_001286630///NM_C	1.61 Brd4	bromodomain containing 4	
85.60844	137.84404	0.007 NM_009274///XM_0065	1.61 Sprk2	serine/arginine-rich protein specific kinase 2	
128.34276	206.58994	0.008 NM_008139	1.61 Gnaq	guanine nucleotide binding protein, alpha q polypeptide	
81.630295	131.2164	0.004 NM_001037136///NM_1	1.61 Agap1	ArfGAP with GTPase domain, ankyrin repeat and PH domain 1	

[Nr12-KO, PBS](i[Nr12-KO, SFN] p	RefSeq Transcript ID	FC PBS:SFN	Gene Symbol	Gene Title	Gene Ontology
227.59846	364.3591	0.008 NM_001122594///XM_0	1.60 <i>Phlpp2</i>	PH domain and leucine rich repeat protein phosphatase 2	0006470 // protein dephosphorylation // not recorded///0008152 // metabolic process // inferre
46.61532	74.62542	0.002 NM_001081342///NM_1	1.60 <i>Gpr133</i>	G protein-coupled receptor 133	0007166 // cell surface receptor signaling pathway // inferred from electronic annotation///0007
175.33382	280.0718	0.010 NM_008608	1.60 <i>Mmp14</i>	matrix metalloproteinase 14 (membrane-inserted)	0001503 // ossification // inferred from genetic interaction///0001525 // angiogenesis // inferrec
169.87717	270.61682	0.009 NM_001252313///NM_C	1.59 <i>Ncor1</i>	nuclear receptor co-repressor 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from
112.20864	178.59636	0.004 NM_001256019///NM_C	1.59 <i>Bmp8a</i>	bone morphogenetic protein 8a	0001503 // ossification // inferred from electronic annotation///0001649 // osteoblast differenti
76.61679	121.892235	0.002 NM_145469///XM_0065	1.59 <i>Nipal2</i>	NIPA-like domain containing 2	0015693 // magnesium ion transport // inferred from electronic annotation
139.39969	221.6585	0.002 NM_001127382///NM_C	1.59 <i>Rbm47</i>	RNA binding motif protein 47	0002244 // hematopoietic progenitor cell differentiation // inferred from mutant phenotype
154.64069	245.34033	0.009 NM_001122989///NM_1	1.59 <i>Cdc14b</i>	CDC14 cell division cycle 14B	0006281 // DNA repair // inferred from electronic annotation///0006470 // protein dephosphory
267.5616	424.32977	0.005 NM_183186///XM_0065	1.59 <i>Foxn3</i>	forkhead box N3	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // reg
50.520676	80.09842	0.004 NM_019588///XM_0065	1.59 <i>Plce1</i>	phospholipase C, epsilon 1	0000187 // activation of MAPK activity // not recorded///0006629 // lipid metabolic process // in
919.9455	1456.9144	0.010 NM_139149///XM_0065	1.58 <i>Fus</i>	fused in sarcoma	0000166 // nucleotide binding // inferred from electronic annotation///0003676 // nucleic acid b
157.5852	249.31615	0.002 NM_138593	1.58 <i>Larp7</i>	La ribonucleoprotein domain family, member 7	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from
33.56851	52.969547	0.002 NM_001081267	1.58 <i>Rsf1</i>	remodeling and spacing factor 1	0006334 // nucleosome assembly // not recorded///0006338 // chromatin remodeling // not rec
214.85323	338.34213	0.004 NM_029735///XM_0064	1.57 <i>Eprs</i>	glutamyl-prolyl-tRNA synthetase	0006412 // translation // inferred from electronic annotation///0006417 // regulation of transl
52.963245	83.01658	0.003 NM_133187///XM_0065	1.57 <i>Fam198b</i>	family with sequence similarity 198, member B	0000139 // Golgi membrane // inferred from electronic annotation///0005794 // Golgi apparatus
302.86575	473.274	0.006 NM_030886///NM_198C	1.56 <i>Ankrd17</i>	ankyrin repeat domain 17	0001955 // blood vessel maturation // inferred from mutant phenotype///0007492 // endoderm
1870.5076	2920.1187	0.005 NM_001093764///NM_C	1.56 <i>Myadm</i>	myeloid-associated differentiation marker	0001933 // negative regulation of protein phosphorylation // not recorded///0010629 // negativ
223.12712	347.63193	0.005 NM_001081203///XM_0	1.56 <i>Sbno1</i>	sno, strawberry notch homolog 1 (Drosophila)	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation///C
72.766525	113.172195	0.001 NM_001109975///NM_1	1.56 <i>Synpo</i>	synaptopodin	0030865 // cortical cytoskeleton organization // non-traceable author statement///0032233 // pr
386.83777	601.2774	0.002 NM_001113545///NM_C	1.55 <i>Lima1</i>	LIM domain and actin binding 1	0030835 // negative regulation of actin filament depolymerization // not recorded///0031529 //
373.1615	578.8367	0.001 NM_001136240///NM_1	1.55 <i>Chdh</i>	choline dehydrogenase	0006066 // alcohol metabolic process // inferred from electronic annotation///0016117 // carote
204.4373	316.90594	0.003 NM_001205173///NM_1	1.55 <i>Ifjo2</i>	intermediate filament family orphan 2	0005198 // structural molecule activity // inferred from electronic annotation
807.49396	1251.062	0.004 NM_010890	1.55 <i>Nedd4</i>	neural precursor cell expressed, developmentally down-regulated 4	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from
343.139	531.0809	0.004 NM_010560	1.55 <i>Il6st</i>	interleukin 6 signal transducer	0005977 // glycogen metabolic process // inferred from mutant phenotype///0006642 // triglyce
268.3768	415.23944	0.010 NM_009621	1.55 <i>Adamts1</i>	a disintegrin-like and metalloproteinase (reprolysin type) with thrombospondin type 1 motif, 1	0001542 // ovulation from ovarian follicle // inferred from mutant phenotype///0001822 // kidn
150.48409	232.54872	0.005 NM_001197321///NM_C	1.55 <i>Foxp1</i>	forkhead box P1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from
219.75166	338.68494	0.001 NM_001252282///NM_C	1.54 <i>Ogdh</i>	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)	0006091 // generation of precursor metabolites and energy // inferred from sequence or structu
61.148697	94.17461	0.009 NM_001081477///XM_0	1.54 <i>Brwd3</i>	bromodomain and WD repeat domain containing 3	0007010 // cytoskeleton organization // not recorded///0008360 // regulation of cell shape // no
2680.0466	4123.3755	0.002 NM_008302	1.54 <i>Hsp90aab1</i>	heat shock protein 90 alpha (cytosolic), class B member 1	0001890 // placenta development // inferred from mutant phenotype///0006457 // protein fold
119.55461	183.71754	0.003 NM_010124	1.54 <i>Eif4ebp2</i>	eukaryotic translation initiation factor 4E binding protein 2	0006417 // regulation of translation // inferred from electronic annotation///0006446 // regulati
520.86615	798.30365	0.007 NM_001291212///NM_C	1.53 <i>Myo18a</i>	myosin XVIIIa	0007030 // Golgi organization // not recorded///0008152 // metabolic process // inferred from e
52.324303	79.931274	0.007 NM_008449	1.53 <i>Kif5c</i>	kinesin family member 5C	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation///C
37.96012	57.955303	0.006 NM_145430///XM_0065	1.53 <i>Fam222b</i>	family with sequence similarity 222, member B	
156.09846	238.06563	0.007 NM_138657///XM_0065	1.53 <i>Socs7</i>	suppressor of cytokine signaling 7	0008286 // insulin receptor signaling pathway // inferred from mutant phenotype///0009968 // r
828.1501	1261.3615	0.009 NM_010123	1.52 <i>Eif3a</i>	eukaryotic translation initiation factor 3, subunit A	0001731 // formation of translation preinitiation complex // inferred from electronic annotation/
178.14966	270.939	0.006 NM_011213///XM_0065	1.52 <i>Ptirf</i>	protein tyrosine phosphatase, receptor type, F	0001960 // negative regulation of cytokine-mediated signaling pathway // not recorded///00064
476.58768	722.8335	0.003 NM_001081251///NM_C	1.52 <i>Pbrm1</i>	polybromo 1	0001890 // placenta development // inferred from mutant phenotype///0001974 // blood vessel
201.07	304.79947	0.008 NM_001161362///NM_1	1.52 <i>Ppp2r3a</i>	protein phosphatase 2, regulatory subunit B'', alpha	0001754 // eye photoreceptor cell differentiation // not recorded///0007525 // somatic muscle c
187.8261	284.68112	0.005 NM_198303///XM_0064	1.52 <i>Eif5b</i>	eukaryotic translation initiation factor 5B	0006184 // GTP catabolic process // inferred from electronic annotation///0006412 // translation
76.257645	115.54268	0.001 NM_001081350///NM_C	1.52 <i>Nol8</i>	nucleolar protein 8	0006260 // DNA replication // not recorded///0006364 // rRNA processing // not recorded///003
103.30395	155.71524	0.007 NM_018785///XM_0064	1.51 <i>Prpf40a</i>	PRP40 pre-mRNA processing factor 40 homolog A (yeast)	0006397 // mRNA processing // inferred from electronic annotation///0007010 // cytoskeleton o
135.39261	203.5406	0.002 NM_011894///XM_0065	1.50 <i>Sh3bp5</i>	SH3-domain binding protein 5 (BTK-associated)	0006469 // negative regulation of protein kinase activity // inferred from direct assay///0006469
402.42963	604.7821	0.009 NM_024452///XM_0065	1.50 <i>Luzp1</i>	leucine zipper protein 1	0003281 // ventricular septum development // inferred from mutant phenotype///0021503 // ne
228.43387	152.31956	0.007 NM_030731///XM_0065	-1.50 <i>Trim23</i>	tripartite motif-containing 23	0006184 // GTP catabolic process // not recorded///0006471 // protein ADP-ribosylation // not r
712.6971	474.83206	0.006 NM_001110159///NM_C	-1.50 <i>Nxt1</i>	NTF2-related export protein 1	0006405 // RNA export from nucleus // inferred from direct assay///0006611 // protein export fr
1723.9908	1145.6034	0.004 NM_001039368///NM_C	-1.50 <i>LOC100862456///Polr2k</i>	DNA-directed RNA polymerases I, II, and III subunit RPABCA4-like///polymerase (RNA) II (DNA directed) polype	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006360 // tra
171.257	113.783104	0.006 NM_001253685///NM_C	-1.51 <i>Dnajc12</i>	DnaJ (Hsp40) homolog, subfamily C, member 12	
74.34266	49.38743	0.001 NM_029942	-1.51 <i>Prelid2</i>	PRELI domain containing 2	0015914 // phospholipid transport // not recorded
30.163132	19.97883	0.001 NM_001080967///NM_2	-1.51 <i>Tmsb15b2///Tmsb15l///Tn</i>	thymosin beta 15b2///thymosin beta 15b like///thymosin beta 15b1	0007010 // cytoskeleton organization // inferred from electronic annotation///0030036 // actin c
1187.7072	784.6771	0.003 NM_016905	-1.51 <i>Galk1</i>	galactokinase 1	0005975 // carbohydrate metabolic process // inferred from electronic annotation///0006012 //
603.0483	397.4583	0.007 NR_024069	-1.52 <i>Smin4</i>	small integral membrane protein 4	0005739 // mitochondrion // inferred from direct assay///0016020 // membrane // inferred from
368.23785	242.32144	0.005 NM_001256100///NM_C	-1.52 <i>Mtlf3</i>	mitochondrial translational initiation factor 3	0001732 // formation of translation initiation complex // not recorded///0006412 // translation /
6832.678	4477.093	0.000 NM_139198	-1.53 <i>Plac8</i>	placenta-specific 8	0008284 // positive regulation of cell proliferation // inferred from direct assay///0009409 // res
291.448	190.22641	0.007 NM_183275///XM_0065	-1.53 <i>Tefm</i>	transcription elongation factor, mitochondrial	0006119 // oxidative phosphorylation // not recorded///0006259 // DNA metabolic process // nc
502.25217	324.984	0.003 NM_007705///XM_0065	-1.55 <i>Cirbp</i>	cold inducible RNA binding protein	0006950 // response to stress // inferred from electronic annotation///0009409 // response to c
415.6489	263.10162	0.008 NM_008776	-1.58 <i>Pafah1b3</i>	platelet-activating factor acetylhydrolase, isoform 1b, subunit 3	0006629 // lipid metabolic process // inferred from electronic annotation///0007283 // spermat
291.0483	183.60161	0.010 NM_027264///XM_0065	-1.59 <i>Zfp715</i>	zinc finger protein 715	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
366.44653	230.66063	0.008 NR_029382///NR_02981	-1.59 <i>Mir17hg///Mir92-1</i>	Mir17 host gene 1 (non-protein coding)///microRNA 92-1	0001701 // in utero embryonic development // inferred from genetic interaction///0002329 // pr
115.03816	72.38381	0.000 NM_001113401///NM_C	-1.59 <i>Eaf2</i>	ELL associated factor 2	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // reg
26.701725	16.769487	0.004 NM_001136059///NM_C	-1.59 <i>Cyp1a1</i>	cytochrome P450, family 1, subfamily a, polypeptide 1	0001666 // response to hypoxia // inferred from electronic annotation///0001889 // liver develo
62.30257	38.85401	0.001 NM_178417	-1.60 <i>Zfp867</i>	zinc finger protein 867	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
7075.0547	4396.1826	0.004 NM_009760	-1.61 <i>Bnip3</i>	BCL2/adenovirus E1B interacting protein 3	0001666 // response to hypoxia // not recorded///0006309 // apoptotic DNA fragmentation // in
18.792166	11.65461	0.001 NM_027054	-1.61 <i>Cst12</i>	cystatin 12	0010466 // negative regulation of peptidase activity // inferred from electronic annotation///001
30.946371	19.152197	0.010 NM_007749	-1.62 <i>Cox7c</i>	cytochrome c oxidase subunit VIIc	1902600 // hydrogen ion transmembrane transport // inferred from electronic annotation
541.4956	334.2564	0.009 NM_001039562///XM_0	-1.62 <i>Ankrd37</i>	ankyrin repeat domain 37	0005515 // protein binding // inferred from physical interaction
219.12213	134.98166	0.007 NM_011943///XM_0065	-1.62 <i>Map2k6</i>	mitogen-activated protein kinase kinase 6	0000165 // MAPK cascade // not recorded///0000165 // MAPK cascade // inferred from physical
252.87946	156.57854	0.001 NM_009944	-1.62 <i>Cox7a1</i>	cytochrome c oxidase subunit VIIa 1	0055114 // oxidation-reduction process // inferred from sequence or structural similarity///1902
337.33157	207.07092	0.001 NM_175016///XM_0065	-1.63 <i>Alkbh2</i>	alkB, alkylaldehyde repair homolog 2 (E. coli)	0006281 // DNA repair // inferred from electronic annotation///0006307 // DNA dealkylation inv
66.03724	40.408676	0.004 NM_001285853///NM_C	-1.63 <i>Matk</i>	megakaryocyte-associated tyrosine kinase	0006468 // protein phosphorylation // inferred from electronic annotation///0016310 // phosph
153.09377	93.59858	0.003 NM_146159	-1.64 <i>Haus3</i>	HAUS augmin-like complex, subunit 3	0006260 // DNA replication // inferred from electronic annotation///0006261 // DNA-dependent
289.38388	175.44807	0.002 NM_018827///XM_0065	-1.65 <i>Cr1f1</i>	cytokine receptor-like factor 1	0001657 // ureteric bud development // inferred from expression pattern///0008284 // positive

[Nrf2-KO, PBS]	[Nrf2-KO, SFN]	p	RefSeq Transcript ID	FC PBS:SFN	Gene Symbol	Gene Title	Gene Ontology
942.3501	557.65533	0.004	NM_026080///XM_0065	-1.69	Mrps24	mitochondrial ribosomal protein S24	0006412 // translation // inferred from sequence or structural similarity
105.44037	60.948776	0.008	NM_001271729///NM_C	-1.73	Tk1	thymidine kinase 1	0001889 // liver development // inferred from electronic annotation///0006260 // DNA replicat
428.62814	240.13652	0.001	NM_027106///XM_0065	-1.78	Avp1	arginine vasopressin-induced 1	0000187 // activation of MAPK activity // inferred from direct assay///0007049 // cell cycle // inf
632.86444	351.0533	0.006	NM_001005223///XM_0	-1.80	Znhit3	zinc finger, HIT type 3	0046872 // metal ion binding // inferred from electronic annotation
67.62999	37.116673	0.001	NM_026358///NR_0281	-1.82	Mgarp	mitochondria localized glutamic acid rich protein	0006626 // protein targeting to mitochondrion // inferred from direct assay///0008089 // antero
129.81496	68.594696	0.003	NM_001109914	-1.89	Apold1	apolipoprotein L domain containing 1	0001525 // angiogenesis // inferred from electronic annotation///0001666 // response to hypoxi
267.1691	136.2508	0.004	NM_001037134///NM_C	-1.96	Ccne2	cyclin E2	0000079 // regulation of cyclin-dependent protein serine/threonine kinase activity // inferred fro
711.34247	361.6959	0.002	NM_030093	-1.97	Snrnp25	small nuclear ribonucleoprotein 25 (U11/U12)	0006397 // mRNA processing // inferred from electronic annotation///0008380 // RNA splicing //
73.92938	35.603764	0.005	NM_173869	-2.08	Stfa2l1	stefin A2 like 1	0010951 // negative regulation of endopeptidase activity // inferred from electronic annotation
53.3571	25.288898	0.001	NM_001289727///NM_C	-2.11	Tmem255a	transmembrane protein 255A	0016020 // membrane // inferred from electronic annotation//0016021 // integral component c
190.04109	88.3881	0.000	NM_025748///XM_0065	-2.15	Adat2	adenosine deaminase, tRNA-specific 2	0002100 // tRNA wobble adenosine to inosine editing // inferred from electronic annotation//00
202.0172	91.759605	0.002	NM_025491///NM_0283	-2.20	Susd3	sushi domain containing 3	0016020 // membrane // inferred from electronic annotation//0016021 // integral component c
49.01388	16.211506	0.006	XM_006528434///XM_0	-3.02	Astx///Astx6///LOC102631	amplified spermatogenic transcripts X encoded///amplified spermatogenic transcripts X encoded 6///	uncharacterized LOC102631953///uncharacterized LOC102640642
48.069675	15.348848	0.004	NM_009484///XM_0065	-3.13	Uty	ubiquitously transcribed tetratricopeptide repeat gene, Y chromosome	0001701 // in utero embryonic development // inferred from mutant phenotype///0003007 // h